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FORM PTO-1390 (REV. 11-2000) U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371

ATTORNEY'S DOCKET NUMBER: REG 203B-US

U.S. APPLICATION NO. (If known, see 37 CFR 1.5): NOT YET KNOWN 09/787835

INTERNATIONAL APPLICATION NO.	INTERNATIONAL FILING DATE	PRIORITY DATE CLAIMED
PCT/US99/22045	September 22, 1999	September 25, 1998

TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using

APPLICANT(S) FOR DO/EO/US: Neil Stahl and George D. Yancopoulos

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. [X] This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. [ ] This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. [X] This is an express request to begin national examination procedures (35 U.S.C. 371(f)). The submission must include items (5), (6), (9) and (21) indicated below.
4. [ ] The US has been elected by the expiration of 19 months from the priority date (Article 31).
5. [X] A copy of the International Application as filed (35 U.S.C. 371(c)(2))
   a. [ ] is attached hereto (required only if not communicated by the International Bureau).
   b. [ ] has been communicated by the International Bureau.
   c. [X] is not required, as the application was filed in the United States Receiving Office (RO/US).
6. [X] An English language translation of the International Application as filed (35 U.S.C. 371(c)(2)).
   a. [ ] is attached hereto.
   b. [X] has been previously submitted under 35 U.S.C. 154(d)(4).
7. [X] Amendments to the claims of the International Aplication under PCT Article 19 (35 U.S.C. 371(c)(3))
   a. [ ] are attached hereto (required only if not communicated by the International Bureau).
   b. [ ] have been communicated by the International Bureau.
   c. [ ] have not been made; however, the time limit for making such amendments has NOT expired.
   d. [X] have not been made and will not be made.
8. [ ] An English language translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371 (c)(3)).
9. [X] An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. [ ] An English lanugage translation of the annexes of the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11 to 20 below concern document(s) or information included:

11. [ ] An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. [ ] An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. [X] A FIRST preliminary amendment.
14. [ ] A SECOND or SUBSEQUENT preliminary amendment.
15. [ ] A substitute specification.
16. [ ] A change of power of attorney and/or address letter.
17. [ ] A computer-readable form of the sequence listing in accordance with PCT Rule 13ter.2 and 35 U.S.C. 1.821 - 1.825.
18. [ ] A second copy of the published international application under 35 U.S.C. 154(d)(4).
19. [ ] A second copy of the English language translation of the international application under 35 U.S.C. 154(d)(4).
20. [ ] Other items or information:

EI799645935US

09/787835

09/787835 .032201

JC08 Rec'd PCT/PTO 22 MAR 2001

U.S. APPLICATION NO. (if known, see 37 CFR 1.5)	INTERNATIONAL APPLICATION NO	ATTORNEY'S DOCKET NUMBER
Not Yet Known	PCT/US99/22045	REG 203B-US

21. ☒ The following fees are submitted:

	CALCULATIONS PTO USE ONLY
BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)):	
Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO **$1000.00**	
International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO **$860.00**	
International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO **$710.00**	
International preliminary examination fee (37 CFR 1.482) paid to USPTO but all claims did not satisfy provisions of PCT Article 33(1)-(4) **$690.00**	
International preliminary examination fee (37 CFR 1.482) paid to USPTO and all claims satisfied provisions of PCT Article 33(1)-(4) **$100.00**	
ENTER APPROPRIATE BASIC FEE AMOUNT =	$ 710.
Surcharge of **$130.00** for furnishing the oath or declaration later than ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492(e)).	$

CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE	
Total claims	25 - 20 =	5	x **$18.00**	$ 90.
Independent claims	- 3 =		x **$80.00**	$
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ **$270.00**	$

TOTAL OF ABOVE CALCULATIONS =	$ 800.
☐ Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2. +	$
SUBTOTAL =	$ 800.
Processing fee of **$130.00** for furnishing the English translation later than ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492(f)).	$
TOTAL NATIONAL FEE =	$ 800.
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). **$40.00** per property +	$
TOTAL FEES ENCLOSED =	$ 800.
Amount to be refunded:	$
charged:	$

a. ☒ A check in the amount of $ 800. to cover the above fees is enclosed.

b. ☐ Please charge my Deposit Account No. _____ in the amount of $ _____ to cover the above fees. A duplicate copy of this sheet is enclosed.

c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 18-0650. A duplicate copy of this sheet is enclosed.

d. ☐ Fees are to be charged to a credit card. **WARNING:** Information on this form may become public. **Credit card information should not be included on this form.** Provide credit card information and authorization on PTO-2038.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137 (a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

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45,636
REGISTRATION NUMBER

Att. Docket No. REG 203B-US

FIRST CLASS MAIL CERTIFICATE
I hereby certify that this document is being deposited with the United States Postal Service on this date as first class mail addressed to: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202.

Bernadette B. Fahey
Bernadette B. Fahey

July 30, 2002
Date

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application Of	:	Neil Stahl, et al.
USSN	:	09/787,835
Int'l File No.:	:	PCT/US99/22045
Int'l File Date:	:	September 22, 1999
For	:	RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING AND USING
Examiner	:	Unknown
Group	:	Unknown

July 30, 2002

Commissioner for Patents
U.S. Patent and Trademark Office
Box Sequence, P.O. Box 2327
Arlington, VA 22202

Transmittal of Sequence Listing

Sir:

In response to the May 30, 2002 Notification of Missing Requirements Under 35 U.S.C. 371 In The United States Designated/Elected Office (DO/EO/US) ("Notification"), Applicants enclose herewith as Exhibit 1: copy of the May 30, 2002, Notification, Exhibit 2: Sequence Listings in paper and computer-readable forms, Exhibit 3: copy of concurrently filed Amendment and Response to May 30, 2002, Notification (without exhibits) for the above-referenced patent application. A

response to the May 30, 2002 Office Communication is due on July 30, 2002, and, therefore, this response is being timely filed.

Applicants direct the subject Sequence Listings submitted herewith be added to the specification.

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 C.F.R §1.821(c) and (e) respectively, are the same. I hereby state that the content of the paper and computer readable copies of the Sequence Listing submitted herewith and referred to herein in accordance with 37 C.F.R. § 1.821(g), contain no new matter.

No fee is deemed necessary for filing this paper. However, if any fees are deemed necessary, the Commissioner is hereby authorized to charge any such fees required by this paper to Deposit Account No. 18-0650.

Respectfully submitted,

Linda O. Palladino

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FIRST CLASS MAIL CERTIFICATE
I hereby certify that this document is being deposited with the United States Postal Service on this date as first class mail addressed to: Commissioner for Patents, United States Patent and Trademark Office, Washington, D.C. 20231.

Bernadette B Fahey
Bernadette B. Fahey

July 30, 2002
Date

Att. Dkt. No. - REG 203B-US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Neil Stahl, et al.		
U.S. Serial No.:	09/787,835	**Examiner:**	Unknown
Int'l File No.:	PCT/US99/22045	**Group Art Unit:**	Unknown
Int'l Filing Date:	September 22, 1999		
Title:	RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING AND USING		

July 30, 2002

Commissioner of Patents
U.S. Patent and Trademark Office
Washington, DC 20231

SIR:

AMENDMENT AND RESPONSE TO MAY 30, 2002, NOTIFICATION OF MISSING REQUIREMENTS UNDER 35 USC 371 IN THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US)

Pursuant to a Notification of Missing Requirements Under 35 U.S.C. 371 in the United States Designated/Elected Office (DO/EO/US) issued on May 30, 2002 ("Notification"), in connection with the above-identified application, Applicants submit herewith as Exhibit A: copy of May 30, 2002, Notification.

Prior to examination of the application on the merits, please amend the specification as follows:

Please replace the paragraph starting on page 6, line 25, with the following:

FIGURES 4A-4B (SEQ ID NO: 7). The amino acid sequence of human gp130-Fc-His6 (SEQ ID NO: 7). Amino acids 1 to 619 are from human gp130 (Hibi et al., Cell 63:1149-1157 (1990). Note that amino acid number 2 has been changed from a Leu to a Val in order to accommodate a Kozak sequence in the coding DNA sequence. The signal peptide of gp130-Fc-His6 has been italicized (amino acids 1 to 22). The Ser-Gly bridge is shown in bold type (amino acids 620, 621). Amino acids 662 to 853 are from the Fc domain of human IgG1 (Lewis, et al., J. Immunol. 151:2829-2838 (1993). (†) mark the two cysteines (amino acids number 632 and 635) of the IgG hinge preceding the Fc that form the inter-chain disulfide bridges that link two Fc domains. The hexahistine tag is shown in bold/italic type (amino acids 854 to 859). (•) shows the position of the STOP codon.

Please replace the paragraph starting on page 7, line 7, through page 8, line 5, with the following:

FIGURE 5 (SEQ ID NO: 8). The amino acid sequence of human IL-6Rα-Fc (SEQ ID NO: 8). Key: Amino acids 1 to 358 are from human IL-6Rα (Yamasaki, et al., Science 241:825-828 (1988). Note that amino acid number 2 has been changed from a Leu to a Val in order to accommodate a Kozak sequence in the coding DNA sequence. The signal peptide of IL-6Rα-Fc has been italicized (amino acids 1 to 19). The Ala-Gly bridge is shown in bold type (amino acids 359, 360). Amino acids 361

to 592 are from the Fc domain of human IgG1 (Lewis et al., J. Immunol. 151:2829-2838 (1993). (†) mark the two cysteines (amino acids number 371 and 374) of the IgG hinge preceding the Fc that form the inter-chain disulfide bridges that link two Fc domains. (•) shows the position of the STOP codon.

Please replace the paragraph starting on page 8, line 17, with the following:

FIGURES 9A-B (SEQ ID NO: 9). Amino acid sequence of gp130-Cγ1 (SEQ ID NO: 9). Key: Amino acids 1 to 619 are from human gp130 (Hibi, et al., Cell 63:1149-1157 (1990). Ser-Gly bridge is shown in bold type. Amino acids 662 to 651 are from the constant region of human IgG1 (Lewis et al., J. Immunol. 151:2829-2838 (1993). (*) shows the position of the STOP codon.

Please replace the paragraph starting on page 8, line 22, with the following:

FIGURE 10 (SEQ ID NO: 10). Amino acid sequence of gp130Δ3fibro (SEQ ID NO: 10). Key: Amino acids 1 to 330 are from human gp130 (Hibi et al., Cell 63:1149-1157 (1990). Other symbols as described in Figures 9A-9B (SEQ ID NO: 9).

Please replace the paragraph starting on page 8, line 26, with the following:

FIGURE 11 (SEQ ID NO: 11). Amino acid sequence of J-CH1 (SEQ ID NO: 11). Key: The Ser-Gly bridge is shown in bold, the J-peptide is shown in italics, the C_H1 domain is underlined.

Please replace the paragraph starting on page 9, line 1, with the following:

FIGURE 12 (SEQ ID NO: 12). Amino acid sequence of Cγ4 (SEQ ID NO: 12). Key: The Ser-Gly bridge is shown in bold type. Amino acids 2 to 239 comprise the Cγ4 sequence.

Please replace the paragraph starting on page 9, line4, with the following:

FIGURE 13 (SEQ ID NO: 13). Amino acid sequence of κ-domain (SEQ ID NO: 13). Key: The Ser-Gly bridge is shown in bold type. Amino acids 2 to 108 comprise the κ domain. The C-terminal cysteine (amino acid 108) is that involved in the disulfide bond of the κ domain with the C_H1 domain of Cγ.

Please replace the paragraph starting on page 9, line 9, with the following:

FIGURE 14 (SEQ ID NO: 14). Amino acid sequence of λ-domain(SEQ ID NO: 14). Key: The Ser-Gly bridge is shown in bold type. Amino acids 2 to 106 comprise the λ domain (Cheung, et al., J. Virol. 66: 6714-6720 (1992). The C-terminal cysteine (amino acid 106) is that involved in the disulfide bond of the λ domain with the C_H1 domain of Cγ.

Please replace the paragraph starting on page 9, line 15, with the following:

FIGURE 15 (SEQ ID NO: 15). Amino acid sequence of the soluble IL-6Rα domain (SEQ ID NO: 15). Key: Amino acids 1 to 358 comprise the soluble IL-6Rα domain (Yamasaki, et al., Science 241:825-828 (1988). The Ala-Gly bridge is shown in bold type.

Please replace the paragraph starting on page 9, line 19, with the following:

FIGURE 16 (SEQ ID NO: 16). Amino acid sequence of the soluble IL-6Rα313 domain (SEQ ID NO: 16): Key: Amino acids 1 to 313 comprise the truncated IL-6Rα domain (IL-6Rα313). The Thr-Gly bridge is shown in bold type.

Please replace the paragraph starting on page 10, line 11, with the following:

FIGURES 19A-19B. IL-6 can induce multimerization of the ligand trap. (Figure 19A) Two different ligand traps are depicted schematically and listed according to their ability to bind protein A. gp130-Fc•IL-6Rα-Fc (GF6F) binds protein A via its Fc-domains, whereas gp130-C_H1•IL-6Rα-k (G16K) does not bind to protein A. (Figure 19B) Anti-kappa western blotting of proteins precipitated with Protein A-Sepharose from mixtures of GF6F ± IL-6, G16K ± IL-6, or GF6F plus G16K ± IL-6, as marked.

Please replace the paragraph starting on page 11, line 1, with the following:

FIGURES 21A-21D (SEQ ID NOS: 17 and 18) - Nucleotide sequence (SEQ ID NO: 17) encoding and deduced amino acid sequence (SEQ ID NO: 18) of fusion polypeptide designated 424 which is capable of binding the cytokine IL-4 to form a nonfunctional complex.

Please replace the paragraph starting on page 11, line 5, with the following:

FIGURES 22A-22D (SEQ ID NOS: 19 and 20) - Nucleotide sequence (SEQ ID NO: 19) encoding and deduced amino acid sequence (SEQ ID NO: 20) of fusion polypeptide designated 603 which is capable of binding the cytokine IL-4 to form a nonfunctional complex.

Please replace the paragraph starting on page 11, line 9, with the following:

FIGURES 23A-23D (SEQ ID NOS: 21 and 22)- Nucleotide sequence (SEQ ID NO: 21) encoding and deduced amino acid sequence (SEQ ID NO:22) of fusion polypeptide designated 622 which is capable of binding the cytokine IL-4 to form a nonfunctional complex.

Please replace the paragraph starting on page 11, line 13, with the following:

FIGURES 24A-24F (SEQ ID NOS: 23 and 24) - Nucleotide sequence (SEQ ID NO: 23) encoding and deduced amino acid sequence (SEQ ID NO: 24) of fusion polypeptide designated 412 which is capable of binding the cytokine IL-6 to form a nonfunctional complex.

Please replace the paragraph starting on page 11, line 17, with the following:

FIGURES 25A-25F (SEQ ID NOS: 25 and 26) - Nucleotide sequence (SEQ ID NO: 25) encoding and deduced amino acid sequence (SEQ ID NO: 26) of fusion polypeptide designated 616 which is capable of binding the cytokine IL-6 to form a nonfunctional complex.

Please replace the paragraph starting on page 11, line 21, with the following:

FIGURES 26A-26E (SEQ ID NOS: 27 and 28)- Nucleotide sequence (SEQ ID NO: 27) encoding and deduced amino acid sequence (SEQ ID NO: 28) of fusion polypeptide designated 569 which is capable of binding the cytokine IL-1 to form a nonfunctional complex.

Please replace the paragraph starting on page 12, line 12, with the following:

FIGURES 31A-31G (SEQ ID NOS: 29 and 30) - The nucleotide (SEQ ID NO: 29) and encoded amino acid (SEQ ID NO: 30) sequence of the IL-4Rα.IL-13Rα1.Fc single chain trap construct is set forth.

Please replace the paragraph starting on page 12, line 15, with the following:

FIGURE 32A-32G (SEQ ID NOS: 31 and 32) - The nucleotide (SEQ ID NO: 31) and encoded amino acid sequence (SEQ ID NO: 32) of the IL-13Rα1.IL-4Rα.Fc single chain trap construct is set forth.

Please replace the paragraph starting on page 42, line 5, with the following:

SF21 insect cells obtained from *Spodoptera frugiperda* were grown at 27C in Gibco SF900 II medium to a density of $1x10^6$ cells/mL. The individual virus stock for either GP130-Fc-His_6 (Figures 4A and 4B [SEQ ID NO: 7]) or IL6Ra-Fc (Figure 5 [SEQ ID NO: 8]) was added to the bioreactor to a low multiplicity 0.01-0.1 PFU/cell to begin the infection. The infection process was allowed to continue for 5-7 days allowing maximum virus replication without incurring substantial cell lysis. The cell suspension was aseptically aliquoted into sterile

centrifuge bottles and the cells removed by centrifugation. The cell-free supernatant was collected in sterile bottles and stored at 4C until further use.

Please replace the paragraph starting on page 49, line 1, through page 51, line 13, with the following:

All the soluble receptor-Ig chimeric genes may be engineered in plasmid vectors including, but not limited to, vectors suitable for mammalian expression (Cos monkey kidney cells, Chinese Hamster Ovary cells [CHO], and ras-transformed fibroblasts [MG-ras]) and include a Kozak sequence (CGC CGC CAC CAT GGT G [SEQ ID NO: 3]) at the beginning of each chimeric gene for efficient translation. Engineering was performed using standard genetic engineering methodology. Each construct was verified by DNA sequencing, mammalian expression followed by western blotting with suitable antibodies, biophysical assays that determine ligand binding and dissociation, and by growth inhibition assays (XG-1, as described later). Since the domains utilized to engineer these chimeric proteins are flanked by appropriate restriction sites, it is possible to use these domains to engineer other chimeric proteins, including chimeras employing the extracellular domains of the receptors for factors such as IL-1, IL-2, IL-3, IL-4, IL-5, GM-CSF, LIF, IL-11, IL-15, IFNγ, TGFβ, and others. The amino acid coordinates for each component utilized in making the IL-6 traps are listed below (Note: numbering starts with the initiating methionine as #1; long sequences are listed using the single letter code for the twenty amino acids):

(a) Constructs employing human gp130:

(i) **gp130-Cγ1** was engineered by fusing in frame the extracellular domain of gp130 (amino acids 1 to 619) to a Ser-Gly bridge, followed by the 330 amino acids which comprise Cγ1 and a termination codon (Figures 9A and 9B [SEQ ID NO: 9]).

(ii) **gp130-J-Cγ1** was engineered in the same manner as gp130-Cγ1 except that a J-peptide (amino acid sequence: GQGTLVTVSS [SEQ ID NO: 4]) was inserted between the Ser-Gly bridge and the sequence of Cγ1 (see Figures 9A and 9B [SEQ ID NO: 9]).

(iii) **gp130Δ3fibro-Cγ1** was engineered by fusing in frame the extracellular domain of gp130 without its three fibronectin-like domains (Figure 10 [SEQ ID NO: 10]). The remaining part of this chimeric protein is identical to gp130-Cγ1.

(iv) **gp130-J-C_H1** was engineered in a manner identical for that described for gp130-Cγ1, except that in place of the Cγ1 region only the C_H1 part of Cγ1 has been used (Figure 11 [SEQ ID NO: 11]). The C-terminal domain of this construct includes the part of the hinge that contains the cysteine residue responsible for heterodimerization of the heavy chain of IgG with a light chain. The part of the hinge that contains the two cysteines involved in Cγ1 homodimerization has been deleted along with the C_H2 and C_H3 domains.

(v) **gp130-Cγ4** was engineered in a manner identical to that described for gp130-Cγ1, except that Cγ4 was used in place of Cγ1 (Figure 12 [SEQ ID NO: 12]). In addition, an *Rsr*II DNA restriction site was engineered at the hinge region of the Cγ4 domain by introducing two silent base mutations. The *Rsrs*II site allows for other desired genetic engineering manipulations, such as the construction of the C_H1 equivalent of gp130-Cγ4.

(vi) **gp130-κ** was engineered in a manner identical to that described for gp130-Cγ1, except that the constant region of the κ light chain of human Ig was used in place of Cγ1 (Figure 13 [SEQ ID NO: 13]).

(vi) **gp130-J-κ** was engineered in a manner identical to that described for gp130-J-κ, except that a j-peptide (amino acid sequence: TFGQGTKVEIK [SEQ ID NO: 5]) was inserted between the Ser-Gly bridge and the κ -region.

(viii) **gp130-λ** was engineered in a manner identical to that described for gp130-Cγ1, except that the constant region of the λ light chain (Cheung, et al., Journal of Virology 66:6714-6720 (1992) of human Ig was used in place of Cγ1 (Figure 14 [SEQ ID NO: 14]).

Constructs employing human IL-6Ra:

(i) **IL6R-Cγ1** was engineered by fusing in frame amino acids 1 to 358 of IL-6Rα (Yamasaki et al., Science 241:825-828 (1988), which comprise the extracellular domain of IL-6Rα (Figure 15 [SEQ ID NO: 15]), to an Ala-Gly bridge, followed by the 330 amino acids which comprise Cγ1 and a termination codon.

(ii) **IL6R-κ** was engineered as described for IL6R-Cγ1, except that the κ-domain (Figure 13 [SEQ ID NO: 13]) utilized for gp130-κ was used in place of Cγ1.

(iii) **IL6R-j-κ** was engineered as described for IL6R-κ except that the j-peptide described for gp130-j-κ was placed between the Ala-Gly bridge and the κ-domain.

(iv) Three additional constructs, **IL6R313-Cγ1**, **IL6R313-κ**, and **IL6R313-j-κ**, were engineered as using a truncated form of IL-6Ra comprised of amino acids 1 to 313 (Figure 16 [SEQ ID NO: 16]). Each of these constructs were made by fusing in frame IL6R313 with a Thr-Gly bridge followed by the Cγ1, κ-, and j-κ-domains described above. These constructs were engineered in order to complement the gp130Δ3fibro-derived constructs.

Please replace the paragraph starting on page 53, line 5, with the following:

In a different set of experiments the ability of the ligand traps to multimerize in the presence of ligand was tested. An example of this is shown on Figures 19A and 19B. IL-6-induced association of gp130-Fc•IL-6Rα-Fc with gp130-C_H1•IL-6Rα-κ was

determined by testing whether gp130-C_H1•IL-6Rα-κ, which does not by itself bind protein A, could be precipitated by protein A-Sepharose in the presence of gp130-Fc•IL-6Rα-Fc in an IL-6-depended manner (Figures 9A and 9B [SEQ ID NO: 9]). Precipitation of gp130-C_H1•IL-6Rα-κ by Protein A-Sepharose was determined by western blotting with an anti-kappa specific HRP conjugate, which does not detect gp130-Fc•IL-6Rα-Fc. gp130-C_H1•IL-6Rα-κ could be precipitated by Protein A-Sepharose only when both gp130-Fc•IL-6Rα-Fc and IL-6 were present. This result conclusively indicates that IL-6 can induce ligand trap multimerization, and further indicate that the ligand trap can mimic the hexameric cytokine•Rα•signal transducer complex (Figure 1). Ligand-induced multimerization may play a significant role in the clearance of cytokine•ligand trap complexes *in vivo*.

Please replace the paragraph starting on page 55, line 12, with the following:

The nucleotide sequences encoding the cytokine traps were constructed from the individual cloned DNAs (described *supra*) by standard cloning and PCR techniques. In each case, the sequences were constructed in frame such that the sequence encoding the first fusion polypeptide component was fused to the sequence encoding the second fusion polypeptide component followed by an Fc domain (hinge, CH2 and CH3 region of human IgG1) as the multimerizing component. In some cases extra nucleotides were inserted in frame between sequences encoding the first and second fusion polypeptide components to add a linker region between the two components (See Figures. 21A-21D [SEQ ID NO: 17] - trap 424; Figures. 24A-24F [SEQ ID NO: 23] - trap 412; and Figures. 26A-26E [SEQ ID NO: 27]- trap 569).

Please replace the paragraph starting on page 55, line 24, with the following:

For the IL-4 traps, 424 (Figures. 21A-21D [SEQ ID NO: 17]), 603 (Figures. 22A-22D [SEQ ID NO: 19]) and 622 (Figures. 23A-23D) [SEQ ID NO: 21], the IL-2Rγ component is 5', followed by the IL4Rα component and then the Fc component. For

the IL-6 traps, 412 (Figures. 24A-24F [SEQ ID NO: 23]) and 616 (Figures. 25A-25F [SEQ ID NO: 25]), the IL-6Rα component is 5' followed by the gp130 component and then the Fc domain. For the IL-1 trap 569 (Figures. 26A-26E [SEQ ID NO: 27] the IL-1RAcP component is 5' followed by the IL-1RI component and then the Fc domain. The final constructs were cloned into the mammalian expression vector pCDNA3.1 (STRATAGENE).

Please replace the paragraph starting on page 56, line 1, with the following:

In the 569 sequence (Figures. 26A-26E [SEQ ID NO: 27]), nucleotides 1-1074 encode the IL1RAcP component, nucleotides 1075 -1098 encode a linker region, nucleotides 1099-2043 encode the IL1RI component and nucleotides 2044-2730 encode the Fc domain.

Please replace the paragraph starting on page 56, line 7, with the following:

In the 412 sequence (Figures. 24A-24F [SEQ ID NO: 23]), nucleotides 1-993 encode the IL6Rα component, nucleotides 994-1023 encode a linker region, nucleotides 1024-2814 encode the gp130 component and nucleotides 2815-3504 encode the Fc domain.

Please replace the paragraph starting on page 56, line 12, with the following:

In the 616 sequence (Figures. 25A-25F [SEQ ID NO: 25]), nucleotides 1-993 encode the IL6Rα component, nucleotides 994-2784 encode the gp130 component and nucleotides 2785-3474 encode the Fc domain.

Please replace the paragraph starting on page 56, line 16, with the following:

In the 424 (Figures. 21A-21D [SEQ ID NO: 17]) and 622 (Figures. 23A-23D [SEQ ID NO: 21]) sequences, nucleotides 1-762 encode the IL2Rγ component, nucleotides 763-771 encode a linker region, nucleotides 772-1395 encode the IL4Rα component and nucleotides 1396-2082 encode the Fc domain.

Please replace the paragraph starting on page 56, line 21, with the following:

Finally, in the 603 sequence (Figures. 22A-22D [SEQ ID NO: 19]), nucleotides 1-762 encode the IL2Rγ component, nucleotides 763-1386 encode the IL4Rα component and nucleotides 1387-2073 encode the Fc domain.

Please replace the paragraph starting on page 62, line 11, with the following:

Figure 29 shows that the IL6 trap (6SC412 IL6R-scb-gpx-FcΔC1) described in Figures. 24A-24F (SEQ ID NOS: 23 and 24) is a better antagonist of IL-6 in the XG1 bioassay than the neutralizing monoclonal antibody to human IL-6 - BE8.

Please replace the paragraph starting on page 63, line 11, with the following:

Figure 30 shows that the trap 569 (Figures 26A - 26E [SEQ ID NOS: 27 and 28[) is able to antagonize the effects of IL-1 and block the IL-6 production from MRC 5 cells upon treatment with IL-1. At a concentration of 10nM, the trap 569 is able to block the production of IL-6 up to an IL-1 concentration of 3nM. In contrast, the IL-1RI.Fc is a much poorer antagonist of IL-1. It is only able to block the effects of IL-1 up to about 10-20 pM. Thus, the trap 569 is approximately 100x better at blocking IL-1 than IL1RI.Fc.

Please replace the paragraph starting on page 63, line 21, through 64, line 7, with the following:

1. To create the IL-13/IL-4 dual trap designated IL-4Rα.IL-13Rα1.Fc, the human IL-4Rα extracellular domain (corresponding to nucleotides #1-693 of Figures 31A - 31G [SEQ ID NO: 29]) and the human IL-13Rα1 extracellular domain (corresponding to nucleotides #700-1665 of Figures 31A - 31G [SEQ ID NO: 29]) were amplified by

standard PCR techniques and ligated into an expression vector pMT21 which contained the human Fc sequence (corresponding to nucleotides #1671-2355 of Figures 31A - 31G [SEQ ID NO: 29]), thus creating a fusion protein consisting of the IL-4Rα , IL-13Rα1, and the hinge, CH2 and CH3 region of human IgG1 from the N to C terminus. In addition, a two amino acid linker (corresponding to nucleotides #694-699 of Figures 31A - 31G [SEQ ID NO: 30]) with the amino acid sequence SerGly was constructed in frame between the IL-4Rα and the IL-13Rα1 and a two amino acid linker (corresponding to nucleotides #1666-1671 of Figures 31A - 31G [SEQ ID NO: 30]) with the amino acid sequence ThrGly was constructed in frame between the IL-13Rα1 and the Fc portion. All sequences were sequence-verified by standard techniques. The IL-4Rα.IL-13Rα1.Fc coding sequence was then subcloned into the expression vector pCDNA3.1 (Stratagene) using standard molecular biology techniques.

Please replace the paragraph starting on page 64, line 9, with the following:

2. To create the IL-13/IL-4 dual trap designated IL-13Rα1.IL-4Rα.Fc, the IL-13Rα1 extracellular domain (corresponding to nucleotides #1-1029 of Figure 32A - Figure 32G [SEQ ID NO: 31]) and the human IL-4Rα (corresponding to nucleotides # 1060-1692 of Figure 32A - Figure 32G [SEQ ID NO: 31]) were amplified by standard PCR techniques and ligated into the expression vector pJFE14, which contains the human Fc sequence (corresponding to nucleotides #1699-2382 of Figure 32A - Figure 32G [SEQ ID NO: 31]) to create a fusion protein consisting of the IL-13Rα1, IL-4Rα, and the hinge, CH2 and CH3 region of human IgG1 from the N to C terminus. In addition, a ten amino acid linker with the amino acid sequence GlyAlaProSerGlyGlyGlyGlyArgPro (SEQ ID NO: 6)(corresponding to nucleotide #1030-1059 of Figure 32A - Figure 32G [SEQ ID NO: 31]) was constructed in frame between the IL-13Rα1 and the IL-4Rα and a two amino acid linker (corresponding to nucleotides #1693-1698 of Figure 32A - Figure 32G [SEQ ID NO: 32]) with the amino acid sequence SerGly was constructed in frame between IL-4Rα and the Fc

portion. All sequences were sequence-verified using standard techniques. The coding sequence of IL-13Rα1.IL-4Rα.Fc was then subcloned into the expression vector pCDNA3.1 (Stratagene) using standard molecular biology techniques.

REMARKS

This amendment is being made merely to conform the specification to the formal drawings that are being submitted herewith and to insert sequence identifiers. The drawing changes and amendment are needed in order to comply with the rules regarding drawings containing multiple views. Applicants submit herewith as Exhibit B: Marked -Up Versions of pages 6, 7, 8, 9, 10, 11, 12, 42, 49, 50, 51, 53, 55, 56, 62, 63, and 64.

Applicants contend that no new matter is introduced by these Amendments and, therefore, respectfully request entry of the Amendments.

Applicants submit herewith as Exhibit C: copy of the Transmittal of Sequence Listing (without exhibits) which is being submitted concurrently.

No fee is deemed necessary in connection with this submission. However, if any fee is deemed necessary, authorization is hereby given to charge the fee to Deposit Account No. 18-0650.

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I hereby certify that this document is being deposited with the United States Postal Service on this date as first class mail addressed to: Commissioner for Patents, United States Patent and Trademark Office, Washington, D.C. 20231.

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Bernadette B. Fahey

July 30, 2002
Date

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Neil Stahl, et al.		
U.S. Serial No.:	09/787,835	**Examiner:**	Unknown
Int'l File No.:	PCT/US99/22045	**Group Art Unit:**	Unknown
Int'l Filing Date:	September 22, 1999		
Title:	RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING AND USING		

July 30, 2002

Commissioner of Patents
U.S. Patent and Trademark Office
Washington, DC 20231

SIR:

AMENDMENT AND RESPONSE TO MAY 30, 2002, NOTIFICATION OF MISSING REQUIREMENTS UNDER 35 USC 371 IN THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US)

Pursuant to a Notification of Missing Requirements Under 35 U.S.C. 371 in the United States Designated/Elected Office (DO/EO/US) issued on May 30, 2002 ("Notification"), in connection with the above-identified application, Applicants submit herewith as Exhibit A: copy of May 30, 2002, Notification.

Prior to examination of the application on the merits, please amend the specification as follows:

Please replace the paragraph starting on page 6, line 25, with the following:

FIGURES 4A-4B (SEQ ID NO: 7). The amino acid sequence of human gp130-Fc-His6 (SEQ ID NO: 7). Amino acids 1 to 619 are from human gp130 (Hibi et al., Cell 63:1149-1157 (1990). Note that amino acid number 2 has been changed from a Leu to a Val in order to accommodate a Kozak sequence in the coding DNA sequence. The signal peptide of gp130-Fc-His_6 has been italicized (amino acids 1 to 22). The Ser-Gly bridge is shown in bold type (amino acids 620, 621). Amino acids 662 to 853 are from the Fc domain of human IgG1 (Lewis, et al., J. Immunol. 151:2829-2838 (1993). (†) mark the two cysteines (amino acids number 632 and 635) of the IgG hinge preceding the Fc that form the inter-chain disulfide bridges that link two Fc domains. The hexahistine tag is shown in bold/italic type (amino acids 854 to 859). (•) shows the position of the STOP codon.

Please replace the paragraph starting on page 7, line 7, through page 8, line 5, with the following:

FIGURE 5 (SEQ ID NO: 8). The amino acid sequence of human IL-6Rα-Fc (SEQ ID NO: 8). Key: Amino acids 1 to 358 are from human IL-6Rα (Yamasaki, et al., Science 241:825-828 (1988). Note that amino acid number 2 has been changed from a Leu to a Val in order to accommodate a Kozak sequence in the coding DNA sequence. The signal peptide of IL-6Rα-Fc has been italicized (amino acids 1 to 19). The Ala-Gly bridge is shown in bold type (amino acids 359, 360). Amino acids 361

to 592 are from the Fc domain of human IgG1 (Lewis et al., J. Immunol. 151:2829-2838 (1993). (†) mark the two cysteines (amino acids number 371 and 374) of the IgG hinge preceding the Fc that form the inter-chain disulfide bridges that link two Fc domains. (•) shows the position of the STOP codon.

Please replace the paragraph starting on page 8, line 17, with the following:

FIGURES 9A-B (SEQ ID NO: 9). Amino acid sequence of gp130-Cγ1 (SEQ ID NO: 9). Key: Amino acids 1 to 619 are from human gp130 (Hibi, et al., Cell 63:1149-1157 (1990). Ser-Gly bridge is shown in bold type. Amino acids 662 to 651 are from the constant region of human IgG1 (Lewis et al., J. Immunol. 151:2829-2838 (1993). (*) shows the position of the STOP codon.

Please replace the paragraph starting on page 8, line 22, with the following:

FIGURE 10 (SEQ ID NO: 10). Amino acid sequence of gp130Δ3fibro (SEQ ID NO: 10). Key: Amino acids 1 to 330 are from human gp130 (Hibi et al., Cell 63:1149-1157 (1990). Other symbols as described in Figures 9A-9B (SEQ ID NO: 9).

Please replace the paragraph starting on page 8, line 26, with the following:

FIGURE 11 (SEQ ID NO: 11). Amino acid sequence of J-CH1 (SEQ ID NO: 11). Key: The Ser-Gly bridge is shown in bold, the J-peptide is shown in italics, the C_H1 domain is underlined.

Please replace the paragraph starting on page 9, line 1, with the following:

FIGURE 12 (SEQ ID NO: 12). Amino acid sequence of Cγ4 (SEQ ID NO: 12). Key: The Ser-Gly bridge is shown in bold type. Amino acids 2 to 239 comprise the Cγ4 sequence.

Please replace the paragraph starting on page 9, line4, with the following:

FIGURE 13 (SEQ ID NO: 13). Amino acid sequence of κ-domain (SEQ ID NO: 13). Key: The Ser-Gly bridge is shown in bold type. Amino acids 2 to 108 comprise the κ domain. The C-terminal cysteine (amino acid 108) is that involved in the disulfide bond of the κ domain with the C_H1 domain of Cγ.

Please replace the paragraph starting on page 9, line 9, with the following:

FIGURE 14 (SEQ ID NO: 14). Amino acid sequence of λ-domain(SEQ ID NO: 14). Key: The Ser-Gly bridge is shown in bold type. Amino acids 2 to 106 comprise the λ domain (Cheung, et al., J. Virol. 66: 6714-6720 (1992). The C-terminal cysteine (amino acid 106) is that involved in the disulfide bond of the λ domain with the C_H1 domain of Cγ.

Please replace the paragraph starting on page 9, line 15, with the following:

FIGURE 15 (SEQ ID NO: 15). Amino acid sequence of the soluble IL-6Rα domain (SEQ ID NO: 15). Key: Amino acids 1 to 358 comprise the soluble IL-6Rα domain (Yamasaki, et al., Science 241:825-828 (1988). The Ala-Gly bridge is shown in bold type.

Please replace the paragraph starting on page 9, line 19, with the following:

FIGURE 16 (SEQ ID NO: 16). Amino acid sequence of the soluble IL-6Rα313 domain (SEQ ID NO: 16): Key: Amino acids 1 to 313 comprise the truncated IL-6Rα domain (IL-6Rα313). The Thr-Gly bridge is shown in bold type.

Please replace the paragraph starting on page 10, line 11, with the following:

FIGURES 19A-19B. IL-6 can induce multimerization of the ligand trap. (Figure 19A) Two different ligand traps are depicted schematically and listed according to their ability to bind protein A. gp130-Fc•IL-6Rα-Fc (GF6F) binds protein A via its Fc-domains, whereas gp130-C_H1•IL-6Rα-k (G16K) does not bind to protein A. (Figure 19B) Anti-kappa western blotting of proteins precipitated with Protein A-Sepharose from mixtures of GF6F ± IL-6, G16K ± IL-6, or GF6F plus G16K ± IL-6, as marked.

Please replace the paragraph starting on page 11, line 1, with the following:

FIGURES 21A-21D (SEQ ID NOS: 17 and 18) - Nucleotide sequence (SEQ ID NO: 17) encoding and deduced amino acid sequence (SEQ ID NO: 18) of fusion polypeptide designated 424 which is capable of binding the cytokine IL-4 to form a nonfunctional complex.

Please replace the paragraph starting on page 11, line 5, with the following:

FIGURES 22A-22D (SEQ ID NOS: 19 and 20) - Nucleotide sequence (SEQ ID NO: 19) encoding and deduced amino acid sequence (SEQ ID NO: 20) of fusion polypeptide designated 603 which is capable of binding the cytokine IL-4 to form a nonfunctional complex.

Please replace the paragraph starting on page 11, line 9, with the following:

FIGURES 23A-23D (SEQ ID NOS: 21 and 22)- Nucleotide sequence (SEQ ID NO: 21) encoding and deduced amino acid sequence (SEQ ID NO:22) of fusion polypeptide designated 622 which is capable of binding the cytokine IL-4 to form a nonfunctional complex.

Please replace the paragraph starting on page 11, line 13, with the following:

FIGURES 24A-24F (SEQ ID NOS: 23 and 24) - Nucleotide sequence (SEQ ID NO: 23) encoding and deduced amino acid sequence (SEQ ID NO: 24) of fusion polypeptide designated 412 which is capable of binding the cytokine IL-6 to form a nonfunctional complex.

Please replace the paragraph starting on page 11, line 17, with the following:

FIGURES 25A-25F (SEQ ID NOS: 25 and 26) - Nucleotide sequence (SEQ ID NO: 25) encoding and deduced amino acid sequence (SEQ ID NO: 26) of fusion polypeptide designated 616 which is capable of binding the cytokine IL-6 to form a nonfunctional complex.

Please replace the paragraph starting on page 11, line 21, with the following:

FIGURES 26A-26E (SEQ ID NOS: 27 and 28)- Nucleotide sequence (SEQ ID NO: 27) encoding and deduced amino acid sequence (SEQ ID NO: 28) of fusion polypeptide designated 569 which is capable of binding the cytokine IL-1 to form a nonfunctional complex.

Please replace the paragraph starting on page 12, line 12, with the following:

FIGURES 31A-31G (SEQ ID NOS: 29 and 30) - The nucleotide (SEQ ID NO: 29) and encoded amino acid (SEQ ID NO: 30) sequence of the IL-4Rα.IL-13Rα1.Fc single chain trap construct is set forth.

Please replace the paragraph starting on page 12, line 15, with the following:

FIGURE 32A-32G (SEQ ID NOS: 31 and 32) - The nucleotide (SEQ ID NO: 31) and encoded amino acid sequence (SEQ ID NO: 32) of the IL-13Rα1.IL-4Rα.Fc single chain trap construct is set forth.

Please replace the paragraph starting on page 42, line 5, with the following:

SF21 insect cells obtained from *Spodoptera frugiperda* were grown at 27C in Gibco SF900 II medium to a density of $1x10^6$ cells/mL. The individual virus stock for either GP130-Fc-His_6 (Figures 4A and 4B [SEQ ID NO: 7]) or IL6Ra-Fc (Figure 5 [SEQ ID NO: 8]) was added to the bioreactor to a low multiplicity 0.01-0.1 PFU/cell to begin the infection. The infection process was allowed to continue for 5-7 days allowing maximum virus replication without incurring substantial cell lysis. The cell suspension was aseptically aliquoted into sterile

centrifuge bottles and the cells removed by centrifugation. The cell-free supernatant was collected in sterile bottles and stored at 4C until further use.

Please replace the paragraph starting on page 49, line 1, through page 51, line 13, with the following:

All the soluble receptor-Ig chimeric genes may be engineered in plasmid vectors including, but not limited to, vectors suitable for mammalian expression (Cos monkey kidney cells, Chinese Hamster Ovary cells [CHO], and ras-transformed fibroblasts [MG-ras]) and include a Kozak sequence (CGC CGC CAC CAT GGT G [SEQ ID NO: 3]) at the beginning of each chimeric gene for efficient translation. Engineering was performed using standard genetic engineering methodology. Each construct was verified by DNA sequencing, mammalian expression followed by western blotting with suitable antibodies, biophysical assays that determine ligand binding and dissociation, and by growth inhibition assays (XG-1, as described later). Since the domains utilized to engineer these chimeric proteins are flanked by appropriate restriction sites, it is possible to use these domains to engineer other chimeric proteins, including chimeras employing the extracellular domains of the receptors for factors such as IL-1, IL-2, IL-3, IL-4, IL-5, GM-CSF, LIF, IL-11, IL-15, IFNγ, TGFβ, and others. The amino acid coordinates for each component utilized in making the IL-6 traps are listed below (Note: numbering starts with the initiating methionine as #1; long sequences are listed using the single letter code for the twenty amino acids):

(a) Constructs employing human gp130:

(i) **gp130-Cγ1** was engineered by fusing in frame the extracellular domain of gp130 (amino acids 1 to 619) to a Ser-Gly bridge, followed by the 330 amino acids which comprise Cγ1 and a termination codon (Figures 9A and 9B [SEQ ID NO: 9]).

(ii) **gp130-J-Cγ1** was engineered in the same manner as gp130-Cγ1 except that a J-peptide (amino acid sequence: GQGTLVTVSS [SEQ ID NO: 4]) was inserted between the Ser-Gly bridge and the sequence of Cγ1 (see Figures 9A and 9B [SEQ ID NO: 9]).

(iii) **gp130Δ3fibro-Cγ1** was engineered by fusing in frame the extracellular domain of gp130 without its three fibronectin-like domains (Figure 10 [SEQ ID NO: 10]). The remaining part of this chimeric protein is identical to gp130-Cγ1.

(iv) **gp130-J-C_H1** was engineered in a manner identical for that described for gp130-Cγ1, except that in place of the Cγ1 region only the C_H1 part of Cγ1 has been used (Figure 11 [SEQ ID NO: 11]). The C-terminal domain of this construct includes the part of the hinge that contains the cysteine residue responsible for heterodimerization of the heavy chain of IgG with a light chain. The part of the hinge that contains the two cysteines involved in Cγ1 homodimerization has been deleted along with the C_H2 and C_H3 domains.

(v) **gp130-Cγ4** was engineered in a manner identical to that described for gp130-Cγ1, except that Cγ4 was used in place of Cγ1 (Figure 12 [SEQ ID NO: 12]). In addition, an *Rsr*II DNA restriction site was engineered at the hinge region of the Cγ4 domain by introducing two silent base mutations. The *Rsrs*II site allows for other desired genetic engineering manipulations, such as the construction of the C_H1 equivalent of gp130-Cγ4.

(vi) **gp130-κ** was engineered in a manner identical to that described for gp130-Cγ1, except that the constant region of the κ light chain of human Ig was used in place of Cγ1 (Figure 13 [SEQ ID NO: 13]).

(vi) **gp130-J-κ** was engineered in a manner identical to that described for gp130-J-κ, except that a j-peptide (amino acid sequence: TFGQGTKVEIK [SEQ ID NO: 5]) was inserted between the Ser-Gly bridge and the κ -region.

(viii) **gp130-λ** was engineered in a manner identical to that described for gp130-Cγ1, except that the constant region of the λ light chain (Cheung, et al., Journal of Virology 66:6714-6720 (1992) of human Ig was used in place of Cγ1 (Figure 14 [SEQ ID NO: 14]).

Constructs employing human IL-6Ra:

(i) **IL6R-Cγ1** was engineered by fusing in frame amino acids 1 to 358 of IL-6Rα (Yamasaki et al., Science 241:825-828 (1988), which comprise the extracellular domain of IL-6Rα (Figure 15 [SEQ ID NO: 15]), to an Ala-Gly bridge, followed by the 330 amino acids which comprise Cγ1 and a termination codon.

(ii) **IL6R-κ** was engineered as described for IL6R-Cγ1, except that the κ-domain (Figure 13 [SEQ ID NO: 13]) utilized for gp130-κ was used in place of Cγ1.

(iii) **IL6R-j-κ** was engineered as described for IL6R-κ except that the j-peptide described for gp130-j-κ was placed between the Ala-Gly bridge and the κ-domain.

(iv) Three additional constructs, **IL6R313-Cγ1**, **IL6R313-κ**, and **IL6R313-j-κ**, were engineered as using a truncated form of IL-6Ra comprised of amino acids 1 to 313 (Figure 16 [SEQ ID NO: 16]). Each of these constructs were made by fusing in frame IL6R313 with a Thr-Gly bridge followed by the Cγ1, κ-, and j-κ-domains described above. These constructs were engineered in order to complement the gp130Δ3fibro-derived constructs.

Please replace the paragraph starting on page 53, line 5, with the following:

In a different set of experiments the ability of the ligand traps to multimerize in the presence of ligand was tested. An example of this is shown on Figures 19A and 19B. IL-6-induced association of gp130-Fc•IL-6Rα-Fc with gp130-C_H1•IL-6Rα-κ was

determined by testing whether gp130-C_H1•IL-6Rα-κ, which does not by itself bind protein A, could be precipitated by protein A-Sepharose in the presence of gp130-Fc•IL-6Rα-Fc in an IL-6-depended manner (Figures 9A and 9B [SEQ ID NO: 9]). Precipitation of gp130-C_H1•IL-6Rα-κ by Protein A-Sepharose was determined by western blotting with an anti-kappa specific HRP conjugate, which does not detect gp130-Fc•IL-6Rα-Fc. gp130-C_H1•IL-6Rα-κ could be precipitated by Protein A-Sepharose only when both gp130-Fc•IL-6Rα-Fc and IL-6 were present. This result conclusively indicates that IL-6 can induce ligand trap multimerization, and further indicate that the ligand trap can mimic the hexameric cytokine•Rα•signal transducer complex (Figure 1). Ligand-induced multimerization may play a significant role in the clearance of cytokine•ligand trap complexes *in vivo*.

Please replace the paragraph starting on page 55, line 12, with the following:

The nucleotide sequences encoding the cytokine traps were constructed from the individual cloned DNAs (described *supra*) by standard cloning and PCR techniques. In each case, the sequences were constructed in frame such that the sequence encoding the first fusion polypeptide component was fused to the sequence encoding the second fusion polypeptide component followed by an Fc domain (hinge, CH2 and CH3 region of human IgG1) as the multimerizing component. In some cases extra nucleotides were inserted in frame between sequences encoding the first and second fusion polypeptide components to add a linker region between the two components (See Figures. 21A-21D [SEQ ID NO: 17] - trap 424; Figures. 24A-24F [SEQ ID NO: 23] - trap 412; and Figures. 26A-26E [SEQ ID NO: 27]- trap 569).

Please replace the paragraph starting on page 55, line 24, with the following:

For the IL-4 traps, 424 (Figures. 21A-21D [SEQ ID NO: 17]), 603 (Figures. 22A-22D [SEQ ID NO: 19]) and 622 (Figures. 23A-23D) [SEQ ID NO: 21], the IL-2Rγ component is 5', followed by the IL4Rα component and then the Fc component. For

the IL-6 traps, 412 (Figures. 24A-24F [SEQ ID NO: 23]) and 616 (Figures. 25A-25F [SEQ ID NO: 25]), the IL-6Rα component is 5' followed by the gp130 component and then the Fc domain. For the IL-1 trap 569 (Figures. 26A-26E [SEQ ID NO: 27] the IL-1RAcP component is 5' followed by the IL-1RI component and then the Fc domain. The final constructs were cloned into the mammalian expression vector pCDNA3.1 (STRATAGENE).

Please replace the paragraph starting on page 56, line 1, with the following:

In the 569 sequence (Figures. 26A-26E [SEQ ID NO: 27]), nucleotides 1-1074 encode the IL1RAcP component, nucleotides 1075 -1098 encode a linker region, nucleotides 1099-2043 encode the IL1RI component and nucleotides 2044-2730 encode the Fc domain.

Please replace the paragraph starting on page 56, line 7, with the following:

In the 412 sequence (Figures. 24A-24F [SEQ ID NO: 23]), nucleotides 1-993 encode the IL6Rα component, nucleotides 994-1023 encode a linker region, nucleotides 1024-2814 encode the gp130 component and nucleotides 2815-3504 encode the Fc domain.

Please replace the paragraph starting on page 56, line 12, with the following:

In the 616 sequence (Figures. 25A-25F [SEQ ID NO: 25]), nucleotides 1-993 encode the IL6Rα component, nucleotides 994-2784 encode the gp130 component and nucleotides 2785-3474 encode the Fc domain.

Please replace the paragraph starting on page 56, line 16, with the following:

In the 424 (Figures. 21A-21D [SEQ ID NO: 17]) and 622 (Figures. 23A-23D [SEQ ID NO: 21]) sequences, nucleotides 1-762 encode the IL2Rγ component, nucleotides 763-771 encode a linker region, nucleotides 772-1395 encode the IL4Rα component and nucleotides 1396-2082 encode the Fc domain.

Please replace the paragraph starting on page 56, line 21, with the following:

Finally, in the 603 sequence (Figures. 22A-22D [SEQ ID NO: 19]), nucleotides 1-762 encode the IL2Rγ component, nucleotides 763-1386 encode the IL4Rα component and nucleotides 1387-2073 encode the Fc domain.

Please replace the paragraph starting on page 62, line 11, with the following:

Figure 29 shows that the IL6 trap (6SC412 IL6R-scb-gpx-FcΔC1) described in Figures. 24A-24F (SEQ ID NOS: 23 and 24) is a better antagonist of IL-6 in the XG1 bioassay than the neutralizing monoclonal antibody to human IL-6 - BE8.

Please replace the paragraph starting on page 63, line 11, with the following:

Figure 30 shows that the trap 569 (Figures 26A - 26E [SEQ ID NOS: 27 and 28[) is able to antagonize the effects of IL-1 and block the IL-6 production from MRC 5 cells upon treatment with IL-1. At a concentration of 10nM, the trap 569 is able to block the production of IL-6 up to an IL-1 concentration of 3nM. In contrast, the IL-1RI.Fc is a much poorer antagonist of IL-1. It is only able to block the effects of IL-1 up to about 10-20 pM. Thus, the trap 569 is approximately 100x better at blocking IL-1 than IL1RI.Fc.

Please replace the paragraph starting on page 63, line 21, through 64, line 7, with the following:

1. To create the IL-13/IL-4 dual trap designated IL-4Rα.IL-13Rα1.Fc, the human IL-4Rα extracellular domain (corresponding to nucleotides #1-693 of Figures 31A - 31G [SEQ ID NO: 29]) and the human IL-13Rα1 extracellular domain (corresponding to nucleotides #700-1665 of Figures 31A - 31G [SEQ ID NO: 29]) were amplified by

standard PCR techniques and ligated into an expression vector pMT21 which contained the human Fc sequence (corresponding to nucleotides #1671-2355 of Figures 31A - 31G [SEQ ID NO: 29]), thus creating a fusion protein consisting of the IL-4Rα , IL-13Rα1, and the hinge, CH2 and CH3 region of human IgG1 from the N to C terminus. In addition, a two amino acid linker (corresponding to nucleotides #694-699 of Figures 31A - 31G [SEQ ID NO: 30]) with the amino acid sequence SerGly was constructed in frame between the IL-4Rα and the IL-13Rα1 and a two amino acid linker (corresponding to nucleotides #1666-1671 of Figures 31A - 31G [SEQ ID NO: 30]) with the amino acid sequence ThrGly was constructed in frame between the IL-13Rα1 and the Fc portion. All sequences were sequence-verified by standard techniques. The IL-4Rα.IL-13Rα1.Fc coding sequence was then subcloned into the expression vector pCDNA3.1 (Stratagene) using standard molecular biology techniques.

Please replace the paragraph starting on page 64, line 9, with the following:

2. To create the IL-13/IL-4 dual trap designated IL-13Rα1.IL-4Rα.Fc, the IL-13Rα1 extracellular domain (corresponding to nucleotides #1-1029 of Figure 32A - Figure 32G [SEQ ID NO: 31]) and the human IL-4Rα (corresponding to nucleotides # 1060-1692 of Figure 32A - Figure 32G [SEQ ID NO: 31]) were amplified by standard PCR techniques and ligated into the expression vector pJFE14, which contains the human Fc sequence (corresponding to nucleotides #1699-2382 of Figure 32A - Figure 32G [SEQ ID NO: 31]) to create a fusion protein consisting of the IL-13Rα1, IL-4Rα, and the hinge, CH2 and CH3 region of human IgG1 from the N to C terminus. In addition, a ten amino acid linker with the amino acid sequence GlyAlaProSerGlyGlyGlyGlyArgPro (SEQ ID NO: 6)(corresponding to nucleotide #1030-1059 of Figure 32A - Figure 32G [SEQ ID NO: 31]) was constructed in frame between the IL-13Rα1 and the IL-4Rα and a two amino acid linker (corresponding to nucleotides #1693-1698 of Figure 32A - Figure 32G [SEQ ID NO: 32]) with the amino acid sequence SerGly was constructed in frame between IL-4Rα and the Fc

portion. All sequences were sequence-verified using standard techniques. The coding sequence of IL-13Rα1.IL-4Rα.Fc was then subcloned into the expression vector pCDNA3.1 (Stratagene) using standard molecular biology techniques.

REMARKS

This amendment is being made merely to conform the specification to the formal drawings that are being submitted herewith and to insert sequence identifiers. The drawing changes and amendment are needed in order to comply with the rules regarding drawings containing multiple views. Applicants submit herewith as Exhibit B: Marked -Up Versions of pages 6, 7, 8, 9, 10, 11, 12, 42, 49, 50, 51, 53, 55, 56, 62, 63, and 64.

Applicants contend that no new matter is introduced by these Amendments and, therefore, respectfully request entry of the Amendments.

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No fee is deemed necessary in connection with this submission. However, if any fee is deemed necessary, authorization is hereby given to charge the fee to Deposit Account No. 18-0650.

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Att. Docket No. REG 203B-US

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Bernadette B. Fahey
Bernadette B. Fahey

December 9, 002
Date

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application Of	:	Neil Stahl, et al.
USSN	:	09/787,835
Int'l File No.:	:	PCT/US99/22045
Int'l File Date:	:	September 22, 1999
For	:	RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING AND USING
Examiner	:	Unknown
Group	:	Unknown

December 9, 2002

Commissioner for Patents
U.S. Patent and Trademark Office
US/DO/EO
BOX PCT
Washington, D.C. 20231

RESPONSE TO NOVEMBER 8, 2002, NOTIFICATION OF DEFECTIVE RESPONSE

Sir:

Applicants are in receipt of a Notification of Defective Response ("Notification") dated November 8, 2002. A response to the November 8, 2002, Notification was originally due on December 8, 2002. However, because December 8, 2002, fell on a Sunday, a response filed the next business day, namely Monday, December 9, 2002, is to be considered timely. Therefore, this response is being filed timely.

Att. Docket No.REG 203B-US
USSN: 09/787,835
Response to November 8, 2002,
Notification of Defective Response

REMARKS

Applicants contend that the November 8, 2002, Notification of Defective Response was sent in error. In support of their contention, Applicants enclose herewith as Exhibit A: copy of the November 8, 2002, Notification, Exhibit B: copy of July 30, 2002, Transmittal of Sequence Listing, including Sequence Listings in paper and computer-readable forms that was submitted to the Commissioner for Patents, U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, Va. 22202, and Exhibit C: copy of return-receipt postcard with PCT/PTO receiving date-stamp of 02 August 2002.

No fee is deemed necessary for filing this paper. However, if any fees are deemed necessary, the Commissioner is hereby authorized to charge any such fees required by this paper to Deposit Account No. 18-0650.

Respectfully submitted,

Linda O. Palladino

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09/787835
JC08 Rec'd PCT/PTO 22 MAR 2001

Att. Dkt. No. - REG 203B-US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Neil Stahl, et al.		
U.S. Serial No.:	Not Yet Known	**Examiner:**	Unknown
Filing Date:	Filed herewith	**Group Art Unit:**	Unknown
Title:	RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING AND USING		

March 22, 2001

Commissioner for Patents
U. S. Patent and Trademark Office
Washington, DC 20231

SIR:

PRELIMINARY AMENDMENT

This paper is submitted in connection with the above-identified U.S. National Stage Patent Application which is being filed concurrently herewith. Prior to examination of the Application on the merits, please amend the specification as follows:

In the specification

Please amend page 1 of the specification to add a priority claim to International Application No. PCT/US99/22045, which was filed on September 22, 1999. Attached herewith, please find a sheet showing a marked up version of corrected page 1 as well as a replacement sheet showing corrected page 1.

Express Mail Label No.EI799645935US

No fee is deemed necessary in connection with filing this Preliminary Amendment. However, if any fee is necessary, authorization is hereby given to charge the amount of any such additional fee to Deposit Account No. 18-0650.

Respectfully submitted,

Linda O. Palladino

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JC08 Rec'd PCT/PTO 22 MAR 2001

RECEPTOR BASED ANTAGONISTS AND METHODS OF MAKING AND USING

This application claims priority of International Application No. PCT US99/22045, filed on September 22, 1999 which claims priority of U.S. Application No. 09/313,942, filed May 19, 1999, which claims priority of U.S. Provisional Application No. 60/101,858 filed September 25, 1998. Throughout this application various publications are referenced. The disclosures of these publications in their entireties are hereby incorporated by reference into this application.

BACKGROUND OF THE INVENTION

Although discovered for varying biological activities, ciliary neurotrophic factor (CNTF), leukemia inhibitory factor (LIF), oncostatin M (OSM) and interleukin-6 (IL-6) comprise a defined family of cytokines (referred to herein as the "CNTF family" of cytokines). These cytokines are grouped together because of their distant structural similarities [Bazan, J. Neuron 7: 197-208 (1991); Rose and Bruce, Proc. Natl. Acad. Sci. USA 88: 8641-8645 (1991)], and, perhaps more importantly, because they share "β" signal-transducing receptor components [Baumann, et al., J. Biol. Chem. 265:19853-19862 (1993); Davis, et al., Science 260: 1805-1808 (1993); Gearing et al., Science 255:1434-1437 (1992); Ip et al., Cell 69: 1121-1132 (1992); Stahl, et al., J. Biol. Chem. 268: 7628-7631 (1993); Stahl and Yancopoulos, Cell 74: 587-590 (1993)]. Receptor activation by this family of cytokines results from either homo- or hetero-dimerization of these β components [Davis, et al. Science 260: 1805-1808 (1993), Murakami, et al., Science 260: 1808-1810 (1993); Stahl and Yancopoulos, Cell 74: 587-590 (1993)]. IL-6 receptor activation requires homodimerization of gp130 [Murakami, et al. Science 260: 1808-1810 (1993), Hibi, et al., Cell 63: 1149-1157 (1990)], a protein initially identified as the IL-6 signal transducer [Hibi, et al., Cell 63: 1149-1157 (1990)]. CNTF, LIF and OSM receptor activation results from heterodimerization between gp130 and a second gp130-related protein known as LIFRβ [Davis,

JC08 Rec'd PCT/PTO 22 MAR 2001

RECEPTOR BASED ANTAGONISTS AND METHODS OF MAKING AND USING

claims priority of International Application No. PCT US99/22045, filed on September 22, 1999 which

This application claims priority of U.S. Application No. 09/313,942, filed May 19, 1999, which claims priority of U.S. Provisional Application No. 60/101,858 filed September 25, 1998. Throughout this application various publications are referenced. The disclosures of these publications in their entireties are hereby incorporated by reference into this application.

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JC20 Rec'd PCT/PTO 13 AUG 2001

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Linda O. Palladino

August 10, 2001
Date

Att. Dkt. No. - REG 203B-US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Neil Stahl, et al.		
U.S. Serial No.:	09/787,835	**Examiner:**	Unknown
Filing Date:	March 22, 2001	**Group Art Unit:**	Unknown
Title:	RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING AND USING		

August 10, 2001

Commissioner of Patents
U.S. Patent and Trademark Office
Washington, DC 20231

SIR:

SECOND PRELIMINARY AMENDMENT

This Second Preliminary Amendment is submitted in connection with the above-identified U.S. National Stage Patent Application. Prior to examination of the Application on the merits, please amend claims 1-10, 12, 15, and 16 and add new claims 26-28 as follows:

1. (Amended) An isolated nucleic acid molecule encoding a fusion polypeptide that forms a multimer capable of binding a cytokine to form a nonfunctional complex, comprising:

a) a nucleotide sequence encoding a first fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the specificity determining component of [the] a cytokine's receptor;

b) a nucleotide sequence encoding a second fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the signal transducing component of [the] a cytokine's receptor; and

c) a nucleotide sequence encoding a third fusion polypeptide component comprising the amino acid sequence of a multimerizing component.

2. (Amended) The nucleic acid molecule of claim 1 or 26, wherein the nucleotide sequence encoding the first component is upstream of the nucleotide sequence encoding the second component.

3. (Amended) The nucleic acid molecule of claim 1 or 26, wherein the nucleotide sequence encoding the first component is downstream of the nucleotide sequence encoding the second component.

4. (Amended) The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a member of the hematopoietin family of cytokines selected from the group consisting of interleukin-2, interleukin-3, interleukin-4, interleukin-5, interleukin-6, interleukin-7, interleukin-9, interleukin-11, interleukin-13, interleukin-15, granulocyte macrophage colony stimulating factor, oncostatin M, and leukemia inhibitory factor and cardiotrophin-1

5. (Amended) The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a member of the interferon family of cytokines selected from the group consisting of IFN-gamma, IFN-alpha, and IFN-beta.

6. (Amended) The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a member of the immunoglobulin superfamily of cytokines selected from the group consisting of B7.1 (CD80) and B7.2 (B70).

7. (Amended). The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a member of the TNF family of cytokines selected from the group consisting of TNF-alpha, TNF-beta, LT-beta, CD40 ligand, Fas ligand, CD 27 ligand, CD 30 ligand, and 4-1BBL.

8. (Amended) The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a member of the TGF-b/BMP family selected from the group consisting of TGF-b1, TGF-b2, TGF-b3, BMP-2, BMP-3a, BMP-3b, BMP-4, BMP-5, BMP-6, BMP-7, BMP-8a, BMP-8b, BMP-9, BMP-10, BMP-11, BMP-15, BMP-16, endometrial bleeding associated factor (EBAF), growth differentiation factor-1 (GDF-1), GDF-2, GDF-3, GDF-5, GDF-6, GDF-7, GDF-8, GDF-9, GDF-12, GDF-14, mullerian inhibiting substance (MIS), activin-1, activin-2, activin-3, activin-4, and activin-5.

9. (Amended) The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a cytokine selected from the group consisting of interleukin-1, interleukin-10, interleukin-12, interleukin-14, interleukin-18 and MIF.

10. (Amended) The isolated nucleic acid molecule of claim 1 or 26, wherein the multimerizing component comprises an immunoglobulin derived domain.

12. (Amended) A fusion polypeptide encoded by the isolated nucleic acid molecule of claim 1 or 26.

15. (Amended) A vector which comprises the nucleic acid molecule of claim 1 or 26.

16. (Amended) An expression vector comprising a nucleic acid molecule of claim 1 or 26, wherein the nucleic acid molecule is operatively linked to an expression control sequence.

26. (New). An isolated nucleic acid molecule encoding a fusion polypeptide that forms a dimer capable of binding a cytokine to form a nonfunctional complex, comprising:

a) a nucleotide sequence encoding a first fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the specificity determining component of [the] a cytokine's receptor;

b) a nucleotide sequence encoding a second fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the signal transducing component of [the] a cytokine's receptor; and

c) a nucleotide sequence encoding a third fusion polypeptide component comprising the amino acid sequence of a multimerizing component.

27. (New) The isolated nucleic acid molecule of claim 1 or 26, wherein the nucleotide sequences of a) and b) are from the same cytokine receptor.

28. (New) The isolated nucleic acid molecule of claim 1 or 26, wherein the nucleotide sequences of a) and b) are from different cytokine receptors.

Marked-up copies of amended claim pages 64-67 are set forth in Exhibit A and Substitute Sheets for amended claim pages 64-67 are set forth in Exhibit B.

No fee is deemed necessary in connection with filing this Second Preliminary Amendment. However, if any fee is necessary, authorization is hereby given to charge the amount of any such additional fee to Deposit Account No. 18-0650.

Respectfully submitted,

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MARKED-UP VERSION

WE CLAIM:

1(amended) An isolated nucleic acid molecule encoding a fusion polypeptide that forms a multimer capable of binding a cytokine to form a nonfunctional complex, comprising:

a) a nucleotide sequence encoding a first fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of ~~the~~ extracellular domain of the specificity determining component of ~~the~~ a cytokine's receptor;

b) a nucleotide sequence encoding a second fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the signal transducing component of ~~the~~ a cytokine's receptor; and

c) a nucleotide sequence encoding a third fusion polypeptide component comprising the amino acid sequence of a multimerizing component.

2.(amended) The nucleic acid molecule of claim 1, or 26 wherein the nucleotide sequence encoding the first component is upstream of the nucleotide sequence encoding the second component.

3.(amended) The nucleic acid molecule of claim 1, or 26 wherein the nucleotide sequence encoding the first component is downstream of the nucleotide sequence encoding the second component.

4.(amended) The isolated nucleic acid molecule of claim 1, or 26 wherein the cytokine receptor is the receptor for a member of the hematopoietin family of cytokines selected from the group consisting of interleukin-2, interleukin-3, interleukin-4, interleukin-5, interleukin-6, interleukin-7, interleukin-9, interleukin-11, interleukin-13, interleukin-15, granulocyte macrophage colony stimulating factor, oncostatin M, and leukemia inhibitory factor and cardiotrophin-1

5.(amended) The isolated nucleic acid molecule of claim 1, or 26 wherein the cytokine receptor is the receptor for a member of the interferon family of cytokines selected from the group consisting of IFN-gamma, IFN-alpha, and IFN-beta.

MARKED-UP VERSION

6(Amended) The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a member of the immunoglobulin superfamily of cytokines selected from the group consisting of B7.1 (CD80) and B7.2 (B70).

7.(Amended) The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a member of the TNF family of cytokines selected from the group consisting of TNF-alpha, TNF-beta, LT-beta, CD40 ligand, Fas ligand, CD 27 ligand, CD 30 ligand, and 4-1BBL.

8.(Amended) The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a member of the TGF-β/BMP family selected from the group consisting of TGF-β1, TGF-β2, TGF-β3, BMP-2, BMP-3a, BMP-3b, BMP-4, BMP-5, BMP-6, BMP-7, BMP-8a, BMP-8b, BMP-9, BMP-10, BMP-11, BMP-15, BMP-16, endometrial bleeding associated factor (EBAF), growth differentiation factor-1 (GDF-1), GDF-2, GDF-3, GDF-5, GDF-6, GDF-7, GDF-8, GDF-9, GDF-12, GDF-14, mullerian inhibiting substance (MIS), activin-1, activin-2, activin-3, activin-4, and activin-5.

9.(Amended) The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a cytokine selected from the group consisting of interleukin-1, interleukin-10, interleukin-12, interleukin-14, interleukin-18 and MIF.

10(Amended) The isolated nucleic acid molecule of claim 1 or 26, wherein the multimerizing component comprises an immunoglobulin derived domain.

11. The isolated nucleic acid molecule of claim 10, wherein the immunoglobulin derived domain is selected from the group consisting of the Fc domain of IgG, the heavy chain of IgG, and the light chain of IgG.

12.(Amended) A fusion polypeptide encoded by the isolated nucleic acid molecule of claim 1 or 26

MARKED-UP VERSION

13. A composition capable of binding a cytokine to form a nonfunctional complex comprising a multimer of the fusion polypeptide of claim 12.

14. The composition of claim 13, wherein the multimer is a dimer.

15. (Amended) A vector which comprises the nucleic acid molecule of claim 1 or 26.

16. (Amended) An expression vector comprising a nucleic acid molecule of claim 1 or 26 wherein the nucleic acid molecule is operatively linked to an expression control sequence.

17. A host-vector system for the production of a fusion polypeptide which comprises the expression vector of claim 16, in a suitable host cell.

18. The host-vector system of claim 17, wherein the suitable host cell is a bacterial cell, yeast cell, insect cell, or mammalian cell.

19. The host-vector system of claim 17, wherein the suitable host cell is E. coli.

20. The host-vector system of claim 17, wherein the suitable host cell is a COS cell.

21. The host-vector system of claim 17, wherein the suitable host cell is a CHO cell.

22. The host-vector system of claim 17, wherein the suitable host cell is a 293 cell.

23. The host-vector system of claim 17, wherein the suitable host cell is a BHK cell.

24. The host-vector system of claim 17, wherein the suitable host cell is a NS0 cell.

MARKED-UP VERSION

25. A method of producing a fusion polypeptide which comprises growing cells of the host-vector system of claim 17, under conditions permitting production of the fusion polypeptide and recovering the fusion polypeptide so produced.

(NEW) 26. An isolated nucleic acid molecule encoding a fusion polypeptide that forms a dimer capable of binding a cytokine to form a nonfunctional complex, comprising:
a) a nucleotide sequence encoding a first fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the specificity determining component of a cytokine's receptor;
b) a nucleotide sequence encoding a second fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the signal transducing component of a cytokine's receptor; and
c) a nucleotide sequence encoding a third fusion polypeptide component comprising the amino acid sequence of a multimerizing component.

27. (NEW) The isolated nucleic acid molecule of claim 1 or 26, wherein the multimerizing component comprises an immunoglobulin derived domain.

28. (NEW) The isolated nucleic acid molecule of claim 1 or 26, wherein the nucleotide sequences of a) and b) are from different cytokine receptors.

SUBSTITUTE SHEET

WE CLAIM:

1. An isolated nucleic acid molecule encoding a fusion polypeptide that forms a multimer capable of binding a cytokine to form a nonfunctional complex, comprising:

a) a nucleotide sequence encoding a first fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the specificity determining component of a cytokine's receptor;

b) a nucleotide sequence encoding a second fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the signal transducing component of a cytokine's receptor; and

c) a nucleotide sequence encoding a third fusion polypeptide component comprising the amino acid sequence of a multimerizing component.

2. The nucleic acid molecule of claim 1 or 26, wherein the nucleotide sequence encoding the first component is upstream of the nucleotide sequence encoding the second component.

3. The nucleic acid molecule of claim 1 or 26, wherein the nucleotide sequence encoding the first component is downstream of the nucleotide sequence encoding the second component.

4. The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a member of the hematopoietin family of cytokines selected from the group consisting of interleukin-2, interleukin-3, interleukin-4, interleukin-5, interleukin-6, interleukin-7, interleukin-9, interleukin-11, interleukin-13, interleukin-15, granulocyte macrophage colony stimulating factor, oncostatin M, and leukemia inhibitory factor and cardiotrophin-1

5. The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a member of the interferon family of cytokines selected from the group consisting of IFN-gamma, IFN-alpha, and IFN-beta.

6. The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a member of the immunoglobulin superfamily of cytokines selected from the group consisting of B7.1 (CD80) and B7.2 (B70).

7. The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a member of the TNF family of cytokines selected from the group consisting of TNF-alpha, TNF-beta, LT-beta, CD40 ligand, Fas ligand, CD 27 ligand, CD 30 ligand, and 4-1BBL.

8. The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a member of the TGF-b/BMP family selected from the group consisting of TGF-b1, TGF-b2, TGF-b3, BMP-2, BMP-3a, BMP-3b, BMP-4, BMP-5, BMP-6, BMP-7, BMP-8a, BMP-8b, BMP-9, BMP-10, BMP-11, BMP-15, BMP-16, endometrial bleeding associated factor (EBAF), growth differentiation factor-1 (GDF-1), GDF-2, GDF-3, GDF-5, GDF-6, GDF-7, GDF-8, GDF-9, GDF-12, GDF-14, mullerian inhibiting substance (MIS), activin-1, activin-2, activin-3, activin-4, and activin-5.

9. The isolated nucleic acid molecule of claim 1 or 26, wherein the cytokine receptor is the receptor for a cytokine selected from the group consisting of interleukin-1, interleukin-10, interleukin-12, interleukin-14, interleukin-18 and MIF.

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13. A composition capable of binding a cytokine to form a nonfunctional complex comprising a multimer of the fusion polypeptide of claim 12.

14. The composition of claim 13, wherein the multimer is a dimer.

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16. An expression vector comprising a nucleic acid molecule of claim 1 or 26, wherein the nucleic acid molecule is operatively linked to an expression control sequence.

17. A host-vector system for the production of a fusion polypeptide which comprises the expression vector of claim 16, in a suitable host cell.

18. The host-vector system of claim 17, wherein the suitable host cell is a bacterial cell, yeast cell, insect cell, or mammalian cell.

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22. The host-vector system of claim 17, wherein the suitable host cell is a 293 cell.

23. The host-vector system of claim 17, wherein the suitable host cell is a BHK cell.

24. The host-vector system of claim 17, wherein the suitable host cell is a NS0 cell.

25. A method of producing a fusion polypeptide which comprises growing cells of the host-vector system of claim 17, under conditions permitting production of the fusion polypeptide and recovering the fusion polypeptide so produced.

26. An isolated nucleic acid molecule encoding a fusion polypeptide that forms a dimer capable of binding a cytokine to form a nonfunctional complex, comprising:

a) a nucleotide sequence encoding a first fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the specificity determining component of a cytokine's receptor;

b) a nucleotide sequence encoding a second fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the signal transducing component of a cytokine's receptor; and

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27. The isolated nucleic acid molecule of claim 1 or 26, wherein the nucleotide sequences of a) and b) are from the same cytokine receptor.

28. The isolated nucleic acid molecule of claim 1 or 26, wherein the nucleotide sequences of a) and b) are from different cytokine receptors.

RECEPTOR BASED ANTAGONISTS AND METHODS OF MAKING AND USING

This application claims priority of U.S. Application No. 09/313,942, filed May 19, 1999, which claims priority of U.S. Provisional Application No. 60/101,858 filed September 25, 1998. Throughout this application various publications are referenced. The disclosures of these publications in their entireties are hereby incorporated by reference into this application.

BACKGROUND OF THE INVENTION

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et al., Science 260: 1805-1808 (1993)], that was initially identified by its ability to bind LIF [Gearing et al., EMBO J. 10: 2839-2848 (1991)].

In addition to the β components, some of these cytokines also require specificity-determining "α" components that are more limited in their tissue distribution than the β components, and thus determine the cellular targets of the particular cytokines [Stahl and Yancopoulos, Cell 74: 587-590 (1993)]. Thus, LIF and OSM are broadly acting factors that may only require the presence of gp130 and LIFRβ on responding cells, while CNTF requires CNTFRα [Stahl and Yancopoulos, Cell 74: 587-590 (1993)] and IL-6 requires IL-6Rα [Kishimoto, et al., Science 258: 593-597 (1992)]. Both CNTFRα (Davis et al., Science 259:1736-1739 (1993) and IL-6Rα [Hibi, et al. Cell 63:1149-1157, Murakami, et al., Science 260:1808-1810 (1990); Taga, et al., Cell 58:573-581 (1989)] can function as soluble proteins, consistent with the notion that they do not interact with intracellular signaling molecules but that they serve to help their ligands interact with the appropriate signal transducing β subunits [Stahl and Yancopoulos, Cell 74: 587-590 (1993)].

Additional evidence from other cytokine systems also supports the notion that dimerization provides a common mechanism by which all cytokine receptors initiate signal transduction. Growth hormone (GH) serves as perhaps the best example in this regard. Crystallographic studies have revealed that each GH molecule contains two distinct receptor binding sites, both of which are recognized by the same binding domain in the receptor, allowing a single molecule of GH to engage two receptor molecules [de Vos, et al., Science 255: 306-312 (1992)]. Dimerization occurs sequentially, with site 1 on the GH first binding to one receptor molecule, followed by the binding of site 2 to a second receptor molecule [Fuh, et al., Science 256: 1677-1680 (1992)]. Studies with the erythropoietin (EPO) receptor are also consistent with the importance of dimerization in receptor activation, as EPO receptors can be constitutively activated by a

single amino acid change that introduces a cysteine residue and results in disulfide-linked homodimers [Watowich, et al., Proc. Natl. Acad. Sci. USA 89:2140-2144 (1992)].

In addition to homo- or hetero-dimerization of β subunits as the critical step for receptor activation, a second important feature is that formation of the final receptor complex by the CNTF family of cytokines occurs through a mechanism whereby the ligand successively binds to receptor components in an ordered manner [Davis, et al. Science 260:1805-1818 (1993); Stahl and Yancopoulos, Cell 74: 587-590 (1993)]. Thus CNTF first binds to CNTFRα, forming a complex which then binds gp130 to form an intermediate (called here the αβ1 intermediate) that is not signaling competent because it has only a single β component, before finally recruiting LIFRβ to form a heterodimer of β components which then initiates signal transduction. Although a similar intermediate containing IL-6 bound to IL-6Rα and a single molecule of gp130 has not been directly isolated, we have postulated that it does exist by analogy to its distant relative, CNTF, as well as the fact that the final active IL-6 receptor complex recruits two gp130 monomers. Altogether, these findings led to a proposal for the structure of a generic cytokine receptor complex (Figure 1) in which each cytokine can have up to 3 receptor binding sites: a site that binds to an optional α specificity-determining component (α site), a site that binds to the first β signal-transducing component (β1 site), and a site that binds to the second β signal-transducing component (β2 site) [Stahl and Yancopoulos, Cell 74: 587-590 (1993)]. These 3 sites are used in sequential fashion, with the last step in complex formation -- resulting in β component dimerization -- critical for initiating signal transduction [Davis, et al. Science 260:1805-1818 (1993)]. Knowledge of the details of receptor activation and the existence of the non-functional β1 intermediate for CNTF has led to the finding that CNTF is a high affinity

antagonist for IL-6 under certain circumstances, and provides the strategic basis for designing ligand or receptor-based antagonists for the CNTF family of cytokines as detailed below.

Once cytokine binding induces receptor complex formation, the dimerization of β components activates intracellular tyrosine kinase activity that results in phosphorylation of a wide variety of substrates [Ip, et al. Cell 69:121-1132 (1992)]. This activation of tyrosine kinase appears to be critical for downstream events since inhibitors that block the tyrosine phosphorylations also prevent later events such as gene inductions [Ip, et al., Cell 69:121-1132 (1992); Nakajima and Wall, Mol. Cell. Biol. 11:1409-1418 (1991)]. Recently, we have demonstrated that a newly discovered family of non-receptor tyrosine kinases that includes Jak1, Jak2, and Tyk2 (referred to as the Jak/Tyk kinases) [Firmbach-Kraft, et al., Oncogene 5:1329-1336 (1990); Wilks, et al., Mol. Cell. Biol. 11: 2057-2065 (1991] and that are involved in signal transduction with other cytokines [Argetsinger, et al., Cell 74:237-244 (1993); Silvennoinen, et al., Proc. Natl. Acad. Sci. USA 90:8429-8433 (1993); Velazquez, et al., Cell 70: 313-322 (1992); Witthuhn, et al., Cell 74:227-236 (1993)], preassociate with the cytoplasmic domains of the β subunits gp130 and LIFRβ in the absence of ligand, and become tyrosine phosphorylated and activated upon ligand addition [Stahl et al., Science 263:92-95 (1994)]. Therefore these kinases appear to be the most proximal step of intracellular signal transduction activated inside the cell as a result of ligand binding outside of the cell. Assay systems for screening collections of small molecules for specific agonist or antagonist activities based on this system are described below.

The CNTF family of cytokines play important roles in a wide variety of physiological processes that provide potential therapeutic applications for both antagonists and agonists.

SUMMARY OF THE INVENTION

An object of the present invention is the production of cytokine antagonists that are useful in the treatment of cytokine-related diseases or disorders.

Another object of the invention is the use of the disclosed cytokine antagonists for the treatment of cytokine-related diseases or disorders. For example, an IL-6 antagonist described herein may be used for the treatment of osteoporosis, the primary and second effects of cancers, including multiple myeloma, or cachexia.

Another object of the invention is the development of screening systems useful for identifying novel agonists and antagonists of cytokine receptors.

Another object of the invention is the development of screening systems useful for identifying small molecules that act as agonists or antagonists of the cytokines.

Another object of the invention is the development of screening systems useful for identifying novel agonists and antagonists of members of the CNTF family of cytokines.

Another object of the invention is the development of screening systems useful for identifying small molecules that act as agonists or antagonists of the CNTF family of cytokines.

BRIEF DESCRIPTION OF THE FIGURES

FIGURE 1: Ordered binding of receptor components in a model of a generic cytokine receptor. The model indicates that cytokines contain up to 3 receptor binding sites and interact with their receptor components by

binding first the optional α component, followed by binding to β1, and then β2. The β components for many cytokine receptors interact through membrane proximal regions (shaded boxes) with the Jak/Tyk family of cytoplasmic protein tyrosine kinases. Only upon dimerization of β components is signal transduction initiated, as schematized by the tyrosine phosphorylations (P) of the β components and the Jak/Tyk kinases.

FIGURE 2: CNTF inhibits IL-6 responses in a PC12 cell line (called PC12D) that expresses IL6Rα, gp130, CNTFRα , but not LIFRβ. Serum-deprived PC12D cells were incubated + IL-6 (50 ng/mL) in the presence or absence of CNTF as indicated. Some plates also received soluble IL6Rα (1 mg/mL) or soluble CNTFRα (1 mg/mL) as indicated. Cell lysates were subjected to immunoprecipitation with anti-gp130 and immunoblotted with anti-phosphotyrosine. Tyrosine phosphorylation of gp130 is indicative of IL-6 induced activation of the IL-6 receptor system, which is blocked upon coaddition of CNTF.

FIGURE 3: Scatchard analysis of iodinated CNTF binding on PC12D cells. PC12D cells were incubated with various concentrations of iodinated CNTF in the presence or absence of excess non-radioactive competitor to determine the specific binding. The figure shows a Scatchard plot of the amount of iodinated CNTF specifically bound, and gives data consistent with two binding sites with dissociation constants of 9 pM and 3.4 nM.

FIGURE 4. The amino acid sequence of human gp130-Fc-His_6. Amino acids 1 to 619 are from human gp130 (Hibi et al., Cell 63:1149-1157 (1990). Note that amino acid number 2 has been changed from a Leu to a Val in order to accommodate a Kozak sequence in the coding DNA sequence. The signal peptide of gp130-Fc-His_6 has been italicized (amino acids 1 to 22). The Ser-Gly bridge is shown in bold type (amino acids 620, 621). Amino acids 662 to 853 are from the Fc domain of human IgG1 (Lewis, et

al., J. Immunol. 151:2829-2838 (1993). (†) mark the two cysteines (amino acids number 632 and 635) of the IgG hinge preceding the Fc that form the inter-chain disulfide bridges that link two Fc domains. The hexahistine tag is shown in bold/italic type (amino acids 854 to 859). (•) shows the position of the STOP codon.

FIGURE 5: The amino acid sequence of human IL-6Rα-Fc. Key: Amino acids 1 to 358 are from human IL-6Rα (Yamasaki, et al., Science 241:825-828 (1988). Note that amino acid number 2 has been changed from a Leu to a Val in order to accommodate a Kozak sequence in the coding DNA sequence. The signal peptide of IL-6Rα-Fc has been italicized (amino acids 1 to 19). The Ala-Gly bridge is shown in bold type (amino acids 359, 360). Amino acids 361 to 592 are from the Fc domain of human IgG1 (Lewis et al., J. Immunol. 151:2829-2838 (1993). (†) mark the two cysteines (amino acids number 371 and 374) of the IgG hinge preceding the Fc that form the inter-chain disulfide bridges that link two Fc domains. (•) shows the position of the STOP codon.

FIGURE 6: The CNTF/IL-6/IL-11 receptor system. The ordered formation of the hexameric signal transducing receptor complex is depicted schematically. The cytokine associates with the Rα component to form an obligatory cytokine•Rα complex (Kd is about 5 nM). This low affinity complex next associates with the first signal transducing component, marked β1, to form a high affinity cytokine•Rα•β1 complex (Kd is about 10 pM). In the case of IL-6Rα, this component is gp130. This trimeric high affinity complex subsequently associates with another such complex. Formation of this complex results in signal transduction as it involves dimerization of two signal transducing components, marked β1 and β2 respectively (adapted from (Ward et al., J. Bio. Chem. 269:23286-23289 (1994); Stahl and Yancopoulos, J. Neurobiology 25:1454-1466 (1994); Stahl and Yancopoulos, Cell 74:587-590 (1993).

FIGURE 7: Design of heterodimeric receptor-based ligand traps for IL-6. The heterodimeric ligand trap is comprised of two interdisulfide linked proteins, gp130-Fc and IL-6Rα-Fc. The gp130-Fc•IL-6Rα-Fc complex (upper panel) is shown to mimic the high affinity cytokine•Rα•β1 complex (lower panel). The ligand trap functions as an antagonist by sequestering IL-6 and thus rendering unavailable to interact with the native receptors on IL-6-responsive cells.

FIGURE 8. Heteromeric immunoglobulin Heavy/Light Chain Receptor Fusions. An example of a heavy/light chain receptor fusion molecule is schematically depicted. The extracellular domain of gp130 is fused to Cγ, whereas the extracellular domain of IL-6Rα is fused to the constant region of the kappa chain (κ). The inter-chain disulfide bridges are also depicted (S-S).

FIGURE 9. Amino acid sequence of gp130-Cγ1. Key: Amino acids 1 to 619 are from human gp130 (Hibi, et al., Cell 63:1149-1157 (1990). Ser-Gly bridge is shown in bold type. Amino acids 662 to 651 are from the constant region of human IgG1 (Lewis et al., J. Immunol. 151:2829-2838 (1993). (*) shows the position of the STOP codon.

FIGURE 10: Amino acid sequence of gp130Δ3fibro. Key: Amino acids 1 to 330 are from human gp130 (Hibi et al., Cell 63:1149-1157 (1990). Other symbols as described in Figure 9.

FIGURE 11: Amino acid sequence of J-CH1. Key: The Ser-Gly bridge is shown in bold, the J-peptide is shown in italics, the C_H1 domain is underlined.

FIGURE 12: Amino acid sequence of Cγ4. Key: The Ser-Gly bridge is shown in bold type. Amino acids 2 to 239 comprise the Cγ4 sequence.

FIGURE 13: Amino acid sequence of κ-domain. Key: The Ser-Gly bridge is shown in bold type. Amino acids 2 to 108 comprise the κ domain. The C-terminal cysteine (amino acid 108) is that involved in the disulfide bond of the κ domain with the C_H1 domain of Cγ.

FIGURE 14: Amino acid sequence of λ-domain. Key: The Ser-Gly bridge is shown in bold type. Amino acids 2 to 106 comprise the λ domain (Cheung, et al., J. Virol. 66: 6714-6720 (1992). The C-terminal cysteine (amino acid 106) is that involved in the disulfide bond of the λ domain with the C_H1 domain of Cγ.

FIGURE 15: Amino acid sequence of the soluble IL-6Rα domain. Key: Amino acids 1 to 358 comprise the soluble IL-6Rα domain (Yamasaki, et al., Science 241:825-828 (1988). The Ala-Gly bridge is shown in bold type.

FIGURE 16: Amino acid sequence of the soluble IL-6Rα313 domain: Key: Amino acids 1 to 313 comprise the truncated IL-6Rα domain (IL-6Rα313). The Thr-Gly bridge is shown in bold type.

FIGURE 17: Purification of gp130-Cγ1•IL-6Rα-κ. 4% to 12% SDS-PAGE gradient gel run under non-reducing conditions. Proteins were visualized by staining with silver. Lane 1: approximately 100 ng of material purified over Protein A Sepharose (Pharmacia). Lane 2: Molecular size standards (Amersham). Lane 3: The Protein A-purified material shown here after further purification over an IL-6 affinity chromatography step. The positions of the gp130-Cγ1 dimer [(gp130-Cγ1)2], the gp130-Cγ1 dimer

associated with one IL-6Rα-κ [(gp130-Cγ1)$_2$•(IL-6Rα-κ)1], and the gp130-Cγ1 dimer associated with two IL-6Rα-κ [(gp130-Cγ1)$_2$•(IL-6Rα-κ)$_2$] are shown, as well as the sizes for the molecular size standards in kilodaltons (200, 100, and 46).

FIGURE 18: IL-6 dissociates slowly from the ligand trap. The dissociation rate of IL-6 from a heavy/light chain receptor-based ligand trap (gp130-Cγ1•IL-6Rα-κ) was compared to that obtained with the neutralizing monoclonal antibody B-E8 (BE8 MAb).

FIGURE 19: IL-6 can induce multimerization of the ligand trap. (A) Two different ligand traps are depicted schematically and listed according to their ability to bind protein A. gp130-Fc•IL-6Rα-Fc (GF6F) binds protein A via its Fc-domains, whereas gp130-C$_H$1•IL-6Rα-κ (G16K) does not bind to protein A. (B) Anti-kappa western blotting of proteins precipitated with Protein A-Sepharose from mixtures of GF6F ± IL-6, G16K ± IL-6, or GF6F plus G16K ± IL-6, as marked.

FIGURE 20: Inhibition of IL-6-dependent XG-1 cell proliferation. XG-1 cells [Zhang, et al., Blood 83:3654-3663 (1994)] were prepared for a proliferation assay by starving the cells from IL-6 for 5 hours. Assays were set up in 96-well tissue culture dishes in RPMI + 10% fetal calf serum + penicillin/streptomycin + 0.050 nM 2-mercaptoethanol + glutamine. 0.1 ml of that media was used per well. Cells were suspended at a density of 250,000 per ml at the start of the assay. 72 hours post addition of IL-6 ± ligands traps or antibodies, an MTT assay was performed as described (Panayotatos et al. Biochemistry 33:5813-5818 (1994). The different ligand traps utilized are listed.

FIGURES 21A-21D: Nucleotide sequence encoding and deduced amino acid sequence of fusion polypeptide designated 424 which is capable of binding the cytokine IL-4 to form a nonfunctional complex.

FIGURES 22A-22D: Nucleotide sequence encoding and deduced amino acid sequence of fusion polypeptide designated 603 which is capable of binding the cytokine IL-4 to form a nonfunctional complex.

FIGURES 23A-23D: Nucleotide sequence encoding and deduced amino acid sequence of fusion polypeptide designated 622 which is capable of binding the cytokine IL-4 to form a nonfunctional complex.

FIGURE 24A-24F: Nucleotide sequence encoding and deduced amino acid sequence of fusion polypeptide designated 412 which is capable of binding the cytokine IL-6 to form a nonfunctional complex.

FIGURE 25A-25F: Nucleotide sequence encoding and deduced amino acid sequence of fusion polypeptide designated 616 which is capable of binding the cytokine IL-6 to form a nonfunctional complex.

FIGURE 26A-26E: Nucleotide sequence encoding and deduced amino acid sequence of fusion polypeptide designated 569 which is capable of binding the cytokine IL-1 to form a nonfunctional complex.

FIGURE 27: Shows that an IL-4 trap designated 4SC375, which is a fusion polypeptide of IL-2Rγ-scb-IL4Rα-FcΔC1, is several orders of magnitude better as an IL-4 antagonist than IL4RαFcΔC1 alone in the TF1 cell bioassay.

FIGURE 28: Shows that an IL-4 trap designated 4SC375 displays antagonistic activity in the TF1 cell bioassay equivalent to an IL-4 trap designated 4SC424 (described in Figs. 21A-21D) which is a fusion

polypeptide of IL-2Rγ-IL4Rα-FcΔC1 having the IL-2Rγ component flush with the IL-4Rα component.

FIGURE 29: Shows that the IL6 trap (6SC412 IL6R-scb-gpx-FcΔC1) described in Figs. 24A-24F is a better antagonist of IL-6 in the XG1 bioassay than the neutralizing monoclonal antibody to human IL-6 - BE8.

FIGURE 30: Shows that the trap 1SC569 (described in Figs. 26A-26E) is able to antagonize the effects of IL-1 and block the IL-6 production from MRC 5 cells upon treatment with IL-1.

FIGURE 31A-31G: The nucleotide and encoded amino acid sequence of the IL-4Rα.IL-13Rα1.Fc single chain trap construct is set forth.

FIGURE 32A-32G: The nucleotide and encoded amino acid sequence of the IL-13Rα1.IL-4Rα.Fc single chain trap construct is set forth.

FIGURE 33: Blocking of IL-13 by IL-4Rα.IL-13Rα1.Fc and IL-13Rα1.IL-4Rα.Fc. Addition of either IL-4Rα.IL-13Rα1.Fc or IL-13Rα1.IL-4Rα.Fc trap at a concentration of 10nM blocks IL-13-induced growth up to ~2nM. At an IL-13 concentration of ~4-5 nM the growth of TF1 cells is inhibited by 50%.

FIGURE 34: Blocking of IL-4 by IL-4Rα.IL-13Rα1.Fc and IL-13Rα1.IL-4Rα.Fc. Addition of either IL-4Rα.IL-13Rα1.Fc or IL-13Rα1.IL-4Rα.Fc at a concentration of 10nM blocks IL-4-induced growth up to ~1nM. At an IL-4 concentration of ~3-4 nM the growth of TF1 cells is inhibited by 50%.

FIGURE 35: Human IL-1 trap blocks the in vivo effects of exogenously administered huIL-1. BALB/c mice were given subcutaneous injection of huIL-1 (0.3 μg/kg) at time 0. Twenty-four hours prior to huIL-1 injection, the animals were pre-treated with either vehicle or 150-fold molar excess

of huIL-1 trap. Two hours prior to sacrifice (26 hrs), the mice were re-challenged with a second injection of huIL-1 (0.3 μg/kg, s.c.). Blood samples were collected at various time points and sera were assayed for IL-1 levels (expressed as mean +/- SEM; n=5 per group).

FIGURE 36A & FIGURE 36B: Human IL-4 trap antagonizes the effects of human IL-4 in monkeys. Figure 36A: Cynomologus monkeys were treated in three parts as indicated. Human IL-4 (25 μg/kg) was injected subcutaneously twice daily for 4 days and human IL-4 trap (8 mg/ml) and vehicle were given intravenously daily for 5 days, beginning 1 day prior to human IL-4 administration. Plasma was collected daily and assayed for MCP-1 levels. Results were expressed as mean +/- SEM; n=4. (ANOVA $p<0.0007$; Tukey-Kramer: Part 2 vs. Part 1, p,0.05; Part 2 vs. Part 3, p,0.05; Part 1 vs. Part 3, not significant.) Figure 36B: Cynomologus monkeys were treated in three parts as indicated. Human IL-4 (25 μg/kg) was injected subcutaneously twice daily for 4 days and human IL-4 trap (8 mg/ml) and vehicle were given intravenously daily for 5 days, beginning 1 day prior to human IL-4 administration. Whole blood was collected daily for flow cytometry analysis for CD16. Results were expressed as mean +/- SEM; n=4. (ANOVA $p<0.042$; Tukey-Kramer: Part 2 vs. Part 1, $p<0.05$; Part 2 vs. Part 3 and Part 1 vs. Part 3, not significant.)

FIGURE 37: Murine IL-4 trap partially prevented IL-4-mediated IgE increase in mice. BALB/C mice injected with anti-mouse IgD (100μl/mouse, s.c.) were randomly divided into 3 groups, each received (on days 3-5) either vehicle, murine IL-4 trap (1 mg/kg, s.c.), or a monoclonal antibody to mouse IL-4 (1 mg/kg, s.c.). Sera were collected at various time points and assayed for IgE levels. Results were expressed as mean+/-SEM (n=5 per group). (ANOVA $p=0.0002$; Tukey-Kramer: vehicle vs. IL-4 trap, $p<0.01$; vehicle vs. IL-4 antibody, $p<0.001$; IL-4 trap vs. IL-4 antibody, not significant).

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides an isolated nucleic acid molecule encoding a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex comprising:

a) a nucleotide sequence encoding a first fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the specificity determining component of the cytokine's receptor;

b) a nucleotide sequence encoding a second fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the signal transducing component of the cytokine's receptor; and

c) a nucleotide sequence encoding a third fusion polypeptide component comprising the amino acid sequence of a multimerizing component.

By "cytokine binding portion" what is meant is the minimal portion of the extracellular domain necessary to bind the cytokine. It is accepted by those of skill in the art that a defining characteristic of a cytokine receptor is the presence of the two fibronectin-like domains that contain canonical cysteines and of the WSXWS box (Bazan, J.F., 1990, PNAS 87: 6934-6938). Sequences encoding the extracellular domains of the binding component of the cytokine's receptor and of the signal transducing component of the cytokine's receptor may also be used to create the fusion polypeptide of the invention. Similarly, longer sequences encoding larger portions of the components of the cytokine's receptor may be used. However, it is contemplated that fragments smaller than the extracellular domain will function to bind the cytokine and therefore, the invention contemplates fusion polypeptides comprising the minimal portion of the extracellular domain necessary to bind the cytokine as the cytokine binding portion.

The invention comprises a "specificity determining component" of a cytokine's receptor and a "signal transducing component" of the cytokine's receptor. Regardless of the nomenclature used to designate a particular component or subunit of a cytokine receptor, one skilled in the art would recognize which component or subunit of a receptor is responsible for determining the cellular target of the cytokine, and thus would know which component constitutes the "specificity determining component."

Similarly, regardless of the nomenclature used, one of skill in the art would know which component or subunit of a receptor would constitute the "signal transducing component." As used herein, the "signal transducing component" is a component of the native receptor which is not the specificity determining component and which does not bind or weakly binds the cytokine in the absence of the specificity determining component. In the native receptor, the "signal transducing component" may participate in signaling.

For example, while some cytokine receptors have components designated α and β, the IL-4 receptor has a signal transducing component referred to as IL-2Rγ. However, regardless of what name is associated with that component, one skilled in the art would know which component of the IL-4 receptor is the signal transducing component. Thus to practice the present invention and create a high affinity trap for IL-4, one of skill in the art would create an isolated nucleic acid comprising a nucleotide sequence encoding a first fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the specificity determining component of the IL-4 receptor (IL-4Rα); a nucleotide sequence encoding a second fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the signal transducing component of the IL-4 receptor (IL-2Rγ); and a nucleotide sequence encoding a third fusion polypeptide component comprising the amino acid sequence of a

multimerizing component (for example, an Fc domain of IgG) to create a high affinity trap for IL-4.

Some further examples of the receptor components that may be used to prepare cytokine antagonists according to the invention are set forth in Table 1. The Table 1 sets forth, by way of example but not by way of limitation, some of the varied nomenclature used in the scientific literature to describe those components which function as specificity determining components and those which function as signal transducing components of certain cytokine receptors.

TABLE 1

Cytokine	Specificity determining Component	Signal transducing Component
Interleukin-1 (IL-1)	Type I IL-1R (ref. 8) Type II IL-1R (ref. 8) IL-1RI (ref. 11) IL-1RII (ref. 11)	IL-1R AcP (refs. 8, 11)
Interleukin-2 (IL-2)	α-subunit (ref. 2) α-chain (ref. 3) IL-2Rα (ref. 1)	β-chain (ref. 3) β-subunit (ref. 2) γ-chain (ref. 3) IL-2Rβ (refs. 1, 10) IL-2Rγ (refs. 1, 10)
Interleukin-3 (IL-3)	IL-3Rα (ref. 1) α-subunit (ref. 2) α-receptor component (ref. 5)	β_c (ref. 1) β-subunit (ref. 2) β-chain (ref. 3) β-receptor component (ref. 5)
Interleukin-4 (IL-4)	IL-4R (ref. 1)	γ-chain (ref. 3) IL-2Rγ (ref. 1)
Interleukin-5 (IL-5)	IL-5Rα (ref. 1) α-subunit (ref. 2) α-receptor component (ref. 5)	β_c (ref. 1) β-subunit (ref. 2) β-chain (ref. 3) β-receptor component (ref. 5)

TABLE 1 (CONT'D)

Cytokine	Specificity determining Component	Signal transducing Component
Granulocyte macrophage-colony stimulating factor (GM-CSF)	α-receptor component (ref. 5) α-subunit (ref. 2) GMRα (refs. 1, 2)	β-receptor component (ref. 5) β-subunit (ref. 2) β-chain (ref. 3) β_c (ref. 1) GMRβ (refs. 1, 2)
Leukemia inhibitory factor (LIF)	LIFBP (ref. 1) α-receptor component (ref. 5)	gp130 (refs. 1, 3) β- receptor component (ref. 5)
Interleukin-11 (IL-11)	α-chain (ref. 4) NR1 (ref. 4)	gp130 (ref. 4)
Interleukin-15 (IL-15)	IL-15Rα (ref. 10)	IL-2Rβ (ref. 10) IL-2Rγ (ref. 10)
Interferon-γ (IFNγ)	IFN-γR (ref. 7) IFN-γR1 (ref. 7)	AF-1 (ref. 7) IFN-γR2 (ref. 7)
TGFβ	Type II (refs. 6, 9)	Type I (refs. 6, 9)

Only a few of the multitude of references are cited in Table 1, and they are set forth as follows:

1. Sato and Miyajima, Current Opinions in Cell Biology 6: 174-179 (1994) - See page 176, lines 9-16;

2. Miyajima, et al., Annual Review of Immunology 10: 295-331 (1992) - See page 295, line 4 to page 296, line 1; page 305, last paragraph;

3. Kondo, et al, Science 262: 1874-1877 (1993) - See page 1874, cols. 1 & 2;

4. Hilton, et al, EMBO Journal 13: 4765-4775 (1994) - See page 4766, col. 1, lines 20 24;

5. Stahl and Yancopoulos, Cell 74: 587-590 (1993) - See page 587, column 2, lines 15-22;

6. Bassing, et al, Journal of Biological Chemistry 269: 14861-14864 (1994) - See page 14861, col. 2, lines 1-9 and 21-28;

7. Kotenko, et al, Journal of Biological Science 270: 20915-20921 (1995) - See page 20915, lines 1-5 of the abstract;

8. Greenfeder, et al., Journal of Biological Chemistry 270: 13757-13765 (1995) - See page 13757, col. 1, line 6 to col. 2, line 3 and col. 2, lines 10-12; page 13764, col. 2, last 3 lines and page 13765, col. 1, lines 1-7;

9. Lebrun and Vale, Molecular Cell Biology 17: 1682-1691 (1997) - See page 1682, Abstract lines 2-6;

10. Kennedy and Park, Journal of Clinical Immunology 16: 134-143 (1996) - See page 134, lines 1-7 of the abstract; page 136, col 2., lines 1-5;

11. Wesche, et al., Journal of Biological Chemistry 272: 7727-7731 (1997) See page 7731, lines 20-26.

Kotenko, et al. recently identified the IL-10R2 (IL-10Rβ) chain which is reported to serve as an accessory chain that is essential for the active IL-10 receptor complex and for initiating IL-10 induced signal transduction events (S.V. Kotenko, et al., The EMBO Journal, 1997, Vol. 16: 5894-5903). Additional cytokines and their receptors are described in Appendix II, page A:9 of Immunobiology, The Immune System In Health and Disease, 2nd

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In preparing the nucleic acid sequence encoding the fusion polypeptide of the invention, the first, second, and third components of the fusion polypeptide are encoded in a single strand of nucleotides which, when expressed by a host vector system, produces a monomeric species of the fusion polypeptide. The monomers thus expressed then multimerize due to the interactions between the multimerizing components (the third fusion polypeptide components). Producing the fusion polypeptides in this manner avoids the need for purification of heterodimeric mixtures that would result if the first and second components were produced as separate molecules and then multimerized. For example, U.S. Patent No. 5,470,952 issued November 28, 1995 describes the production of heterodimeric proteins that function as CNTF or IL-6 antagonists. The heterodimers are purified from cell lines cotransfected with the appropriate alpha (α) and beta (β) components. Heterodimers are then separated from homodimers using methods such as passive elution from preparative, nondenaturing polyacrylamide gels or by using high pressure cation exchange chromatography. The need for this purification step is avoided by the methods of the present invention.

In addition, PCT International Application WO 96/11213 published 18 April 1996 entitled Dimeric IL-4 Inhibitors states that the applicant has prepared homodimers in which two IL-4 receptors are bound by a polymeric spacer and has prepared heterodimers in which an IL-4 receptor is linked by a polymeric spacer to an IL-2 receptor gamma chain. The polymeric spacer described is polyethylene glycol (PEG). The two receptor components, IL-4R and IL-2Rgamma are separately expressed and purified. Pegylated homodimers and heterodimers are then produced by joining the components together using bi-functional PEG reagents. It is an advantage

of the present invention that it avoids the need for such time consuming and costly purification and pegylation steps.

In one embodiment of the invention, the nucleotide sequence encoding the first component is upstream of the nucleotide sequence encoding the second component. In another embodiment of the invention, the nucleotide sequence encoding the first component is downstream of the nucleotide sequence encoding the second component. Further embodiments of the invention may be prepared in which the order of the first, second and third fusion polypeptide components are rearranged. For example, if the nucleotide sequence encoding the first component is designated 1, the nucleotide sequence encoding the second component is designated 2, and the nucleotide sequence of the third component is designated 3, then the order of the components in the isolated nucleic acid of the invention as read from 5′ to 3′ may be any of the following six combinations: 1,2,3; 1,3,2; 2,1,3; 2,3,1; 3,1,2; or 3,2,1.

In further embodiments of the invention, the cytokine bound by the fusion polypeptide may be a member of the hematopoietin family of cytokines selected from the group consisting of interleukin-2, interleukin-3, interleukin-4, interleukin-5, interleukin-6, interleukin-7, interleukin-9, interleukin-11, interleukin-13, interleukin-15, granulocyte macrophage colony stimulating factor, oncostatin M, leukemia inhibitory factor, and cardiotrophin-1.

In additional embodiments of the invention, the cytokine bound by the fusion polypeptide may be a member of the interferon family of cytokines selected from the group consisting of IFN-gamma, IFN-alpha, and IFN-beta.

In additional embodiments of the invention, the cytokine bound by the fusion polypeptide may be a member of the immunoglobulin superfamily

of cytokines selected from the group consisting of B7.1 (CD80) and B7.2 (B70).

In still further embodiments of the invention, the cytokine bound by the fusion polypeptide may be a member of the TNF family of cytokines selected from the group consisting of TNF-alpha, TNF-beta, LT-beta, CD40 ligand, Fas ligand, CD 27 ligand, CD 30 ligand, and 4-1BBL.

In additional embodiments of the invention, the cytokine bound by the fusion polypeptide may be a cytokine selected from the group consisting of interleukin-1, interleukin-10, interleukin-12, interleukin-14, interleukin-18, and MIF.

Because specificity determination and signal transduction occurs by a similar mechanism in the TGF-β/BMP family of cytokines (See D. Kingsley, Genes & Development, 1994, 8: 133-146; J. Wrana, Miner Electrolyte Metab, 24: 120-130 (1998); R. Derynck and X. Feng, Biochimica et Biophysica Acta 1333 (1997) F105-F150; and J. Massague and F. Weis-Garcia, "Serine/threonine Kinase Receptors: Mediators of Transforming Growth Factor Beta Family Signals" In Cancer Surveys, Vol. 27: Cell Signaling, 1996, Imperial Cancer Research Fund) the present invention may be used to produce high affinity antagonists for cytokines that are members of the TGF-β/BMP family.

Therefore, in additional embodiments of the invention, the cytokine bound by the fusion polypeptide may be a member of the TGF-β/BMP family selected from the group consisting of TGF-β1, TGF-β2, TGF-β3, BMP-2, BMP-3a, BMP-3b, BMP-4, BMP-5, BMP-6, BMP-7, BMP-8a, BMP-8b, BMP-9, BMP-10, BMP-11, BMP-15, BMP-16, endometrial bleeding associated factor (EBAF), growth differentiation factor-1 (GDF-1), GDF-2, GDF-3, GDF-5, GDF-6, GDF-7, GDF-8, GDF-9, GDF-12, GDF-14, mullerian

inhibiting substance (MIS), activin-1, activin-2, activin-3, activin-4, and activin-5.

In alternative embodiments of the invention, the specificity determining component, the signal transducing component, or both, may be substituted for by a single chain Fv. A single chain Fv (scFv) is a truncated Fab having only the V region of a heavy chain linked by a stretch of synthetic peptide to a V region of a light chain. See, for example, US Patent Nos. 5,565,332; 5,733,743; 5,837,242; 5,858,657; and 5,871,907 assigned to Cambridge Antibody Technology Limited incorporated by reference herein. Thus the present invention contemplates, for example, an isolated nucleic acid molecule encoding a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex comprising a nucleotide sequence encoding a first fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the specificity determining component of the cytokine's receptor; a nucleotide sequence encoding a second fusion polypeptide component comprising the amino acid sequence of an scFv capable of binding the cytokine at a site different from the site at which the cytokine binding portion of the extracellular domain of the specificity determining component of the cytokine's receptor binds; and a nucleotide sequence encoding a third fusion polypeptide component comprising the amino acid sequence of a multimerizing component. Alternatively, the specificity determining component may be substituted for by a scFv that binds to a site on the cytokine different from the site at which the signal transducing component binds. Thus the invention contemplates an isolated nucleic acid molecule encoding a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex comprising a nucleotide sequence encoding a first fusion polypeptide component comprising the amino acid sequence of a scFv that binds to a site on the cytokine different from the site at which the cytokine binding portion of the extracellular domain of the signal transducing component of the cytokine's receptor binds; a nucleotide sequence encoding a second fusion polypeptide component

comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the signal transducing component of the cytokine's receptor; and a nucleotide sequence encoding a third fusion polypeptide component comprising the amino acid sequence of a multimerizing component.

In another embodiment, the invention contemplates an isolated nucleic acid molecule encoding a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex comprising a nucleotide sequence encoding a first fusion polypeptide component comprising the amino acid sequence of a first scFv that binds to a site on the cytokine; a nucleotide sequence encoding a second fusion polypeptide component comprising the amino acid sequence a second scFv that binds to a site on the cytokine different from the site at which the first scFv binds; and a nucleotide sequence encoding a third fusion polypeptide component comprising the amino acid sequence of a multimerizing component.

In all of the above described embodiments comprising scFv's, the invention also contemplates embodiments in which the nucleotide sequence encoding the first component is upstream of the nucleotide sequence encoding the second component; embodiments in which the nucleotide sequence encoding the first component is downstream of the nucleotide sequence encoding the second component; and further embodiments of the invention in which the order of the first, second and third fusion polypeptide components is rearranged. For example, if the nucleotide sequence encoding the first component is designated 1, the nucleotide sequence encoding the second component is designated 2, and the nucleotide sequence of the third component is designated 3, then the order of the components in the isolated nucleic acid of the invention as read from 5′ to 3′ may be any of the following six combinations: 1,2,3; 1,3,2; 2,1,3; 2,3,1; 3,1,2; or 3,2,1.

In preferred embodiments of the invention, the multimerizing component comprises an immunoglobulin derived domain. More specifically, the immunoglobulin derived domain may be selected from the group consisting of the Fc domain of IgG, the heavy chain of IgG, and the light chain of IgG. In another embodiment, the multimerizing component may be an Fc domain from which the first five amino acids (including a cysteine) have been removed to produce a multimerizing component referred to as Fc(ΔC1). Alternatively, the multimerizing component may be an Fc domain in which a cysteine within the first five amino acids has been substituted for by another amino acid such as, for example, serine or alanine.

The present invention also provides for fusion polypeptides encoded by the isolated nucleic acid molecules of the invention. Preferably, the fusion polypeptides are in multimeric form, due to the function of the third multimerizing component. In a preferred embodiment, the multimer is a dimer. Suitable multimerizing components are sequences encoding an immunoglobulin heavy chain hinge region (Takahashi et al., 1982, Cell 29:671-679); immunoglobulin gene sequences, and portions thereof. In a preferred embodiment of the invention, immunoglobulin gene sequences, especially one encoding the Fc domain, are used to encode the third multimerizing component.

The present invention also contemplates a vector which comprises the nucleic acid molecule of the invention as described herein.

Also provided is an expression vector comprising a nucleic acid molecule of the invention as described herein, wherein the nucleic acid molecule is operatively linked to an expression control sequence. Also provided is a host-vector system for the production of a fusion polypeptide which comprises the expression vector of the invention which has been introduced into a host cell suitable for expression of the fusion

polypeptide. The suitable host cell may be a bacterial cell such as E. coli, a yeast cell, such as Pichia pastoris, an insect cell, such as Spodoptera frugiperda, or a mammalian cell, such as a COS, CHO, 293, BHK or NS0 cell.

The present invention also provides for methods of producing the fusion polypeptides of the invention by growing cells of the host-vector systems described herein, under conditions permitting production of the fusion polypeptide and recovering the fusion polypeptide so produced.

The present invention provides novel antagonists which are based on receptor components that are shared by cytokines such as the CNTF family of cytokines.

The invention described herein contemplates the production of antagonists to any cytokine that utilizes an α specificity determining component which, when combined with the cytokine, binds to a first β signal transducing component to form a nonfunctional intermediate which then binds to a second β signal transducing component causing β-receptor dimerization and consequent signal transduction. According to the invention, the soluble α specificity determining component of the receptor (sRα) and the extracellular domain of the first β signal transducing component of the cytokine receptor (β1) are combined to form heterodimers (sRα:β1) that act as antagonists to the cytokine by binding the cytokine to form a nonfunctional complex.

As described in Example 1, CNTF and IL-6 share the β1 receptor component gp130. The fact that CNTF forms an intermediate with CNTFRα and gp130 can be demonstrated (Example 1) in cells lacking LIFRβ, where the complex of CNTF and CNTFRα binds gp130, and

prevents homodimerization of gp130 by IL-6 and IL-6Rα, thereby blocking signal transduction. These studies provide the basis for the development of the IL-6 antagonists described herein, as they show that if, in the presence of a ligand, a nonfunctional intermediate complex, consisting of the ligand, its α receptor component and its β1 receptor component, can be formed, it will effectively block the action of the ligand. Other cytokines may use other β1 receptor components, such as LIFRβ, which may also be used to produce antagonists according to the present invention.

Thus for example, in one embodiment of the invention, effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the α specificity determining components of their receptors (sIL-6Rα and sCNTFRα, respectively) and the extracellular domain of gp130. The resultant heterodimers, which are referred to hereinafter as sIL-6Rα:β1 and sCNTFRα:β1, respectively, function as high-affinity traps for IL-6 or CNTF, respectively, thus rendering the cytokine inaccessible to form a signal transducing complex with the native membrane-bound forms of their receptors.

Although soluble ligand binding domains from the extracellular portion of receptors have proven to be somewhat effective as traps for their ligands and thus act as antagonists [Bargetzi, et al., Cancer Res. 53:4010-4013 (1993); , et al., Proc. Natl. Acad. Sci. USA 89: 8616-8620 (1992); Mohler, et al., J. Immunol. 151: 1548-1561 (1993); Narazaki, et al., Blood 82: 1120-1126 (1993)], the IL-6 and CNTF receptors are unusual in that the α receptor components constitute ligand binding domains that, in concert with their ligands, function effectively in soluble form as receptor agonists [Davis, et al. Science 259:1736-1739 (1993); Taga, et al., Cell 58: 573-581 (1989)]. The sRα:β1 heterodimers prepared according to the present invention provide effective traps for their ligands, binding these ligands with affinities in the picomolar range (based on binding studies for CNTF to PC12D cells)

without creating functional intermediates. The technology described herein may be applied to develop a cytokine trap for any cytokine that utilizes an α-component that confers specificity, as well as a β component which, when bound to the α–specificity component, has a higher affinity for the cytokine than either component alone. Accordingly, antagonists according to the invention include antagonists of interleukins 1 through 5 [IL-1, Greenfeder, et al. J. Biol. Chem. 270:13757-13765 (1995); Guo, et al. J. Biol. Chem. 270:27562-27568 (1995)], IL-2; [Taniguchi, et al. European Patent Nos. 0386289-A and 0386304-A (1990); Takeshita, et al. Science 257:379-382 (1992)]; IL-3; [Kitamura, et al. Cell 66:1165-1174 (1991)], IL-4; [Idzerda, et al. J. Exp. Med. 171:861-873 (1990)], IL-5; [Taverneir, et al. Cell 66:1175-1184 (1991)], IL-11 [(Cherel, et al. Direct Submission to EMBL/GenBank/DDBJ databases; accession No. Z38102)], interleukin 15 [IL-15; Hemar, et al. J. Cell Biol. 1295:55-64 (1995); Taniguchi, et al. European Patent Nos. 0386289-A and 0386304-A (1990); Takeshita, et al. Science 257:379-382 (1992)], granulocyte-macrophage colony stimulating factor [GM-CSF; Hayashida, et al. Proc. Natl. Acad. Sci. U.S.A. 97:9655-9659 (1990)], LIF, gamma interferon [IFNγ; Aguet, et al. Cell 55:273-280 (1988); Soh, et al. Cell 76:793-802 (1994)], and transforming growth factor beta [TGFβ; Inagaki, et al. Proc. Natl. Acad. Sci. USA 90:5359-5363 (1993)].

The α and β receptor extracellular domains may be prepared using methods known to those skilled in the art. The CNTFRα receptor has been cloned, sequenced and expressed [Davis, et al. (1991) Science 253:59-63 which is incorporated by reference in its entirety herein]. The cloning of LIFRβ and gp130 are described in Gearing et al. in EMBO J. 10:2839-2848 (1991), Hibi, et al. Cell 63:1149-1157 (1990) and in published PCT application WO 93/10151 published May 27, 1993, all of which are incorporated by reference in their entirety herein.

The receptor molecules useful for practicing the present invention may be prepared by cloning and expression in a prokaryotic or eukaryotic expression system. The recombinant receptor gene may be expressed and purified utilizing any number of methods. The gene encoding the factor may be subcloned into a bacterial expression vector, such as for example, but not by way of limitation, pCP110.

The recombinant factors may be purified by any technique which allows for the subsequent formation of a stable, biologically active protein. For example, and not by way of limitation, the factors may be recovered from cells either as soluble proteins or as inclusion bodies, from which they may be extracted quantitatively by 8M guanidinium hydrochloride and dialysis. In order to further purify the factors, conventional ion exchange chromatography, hydrophobic interaction chromatography, reverse phase chromatography or gel filtration may be used.

The sRα:β heterodimeric receptors may be engineered using known fusion regions, as described in published PCT application WO 93/10151 published May 27, 1993 entitled "Receptor for Oncostatin M and Leukemia Inhibitory Factor" which describes production of β receptor heterodimers, or they may be prepared by crosslinking of extracellular domains by chemical means. The domains utilized may consist of the entire extracellular domain of the α and β components, or they may consist of mutants or fragments thereof that maintain the ability to form a complex with its ligand and other components in the sRα:β1 complex. For example, as described below in Example 4, IL-6 antagonists have been prepared using gp130 that is lacking its three fibronectin-like domains.

In one embodiment of the invention, the extracellular domains are engineered using leucine zippers. The leucine zipper domains of the human transcription factors c-jun and c-fos have been shown to form stable heterodimers [Busch and Sassone-Corsi, Trends Genetics 6: 36-40

(1990); Gentz, et al., Science 243: 1695-1699 (1989)] with a 1:1 stoichiometry. Although jun-jun homodimers have also been shown to form, they are about 1000-fold less stable than jun-fos heterodimers. Fos-fos homodimers have not been detected.

The leucine zipper domain of either c-jun or c-fos are fused in frame at the C-terminus of the soluble or extracellular domains of the above mentioned receptor components by genetically engineering chimeric genes. The fusions may be direct or they may employ a flexible linker domain, such as the hinge region of human IgG, or polypeptide linkers consisting of small amino acids such as glycine, serine, threonine or alanine, at various lengths and combinations. Additionally, the chimeric proteins may be tagged by His-His-His-His-His-His (His6),[SEQ. ID NO. 1] to allow rapid purification by metal-chelate chromatography, and/or by epitopes to which antibodies are available, to allow for detection on western blots, immunoprecipitation, or activity depletion/blocking in bioassays.

In another embodiment, as described below in Example 3, the sRα:β1 heterodimer is prepared using a similar method, but using the Fc-domain of human IgG1 [Aruffo, et al., Cell 67:35-44 (1991)]. In contrast to the latter, formation of heterodimers must be biochemically achieved, as chimeric molecules carrying the Fc-domain will be expressed as disulfide-linked homodimers. Thus, homodimers may be reduced under conditions that favor the disruption of inter-chain disulfides but do not effect intra-chain disulfides. Then monomers with different extracellular portions are mixed in equimolar amounts and oxidized to form a mixture of homo- and heterodimers. The components of this mixture are separated by chromatographic techniques. Alternatively, the formation of this type of heterodimers may be biased by genetically engineering and expressing molecules that consist of the soluble or extracellular portion of the receptor components followed by the Fc-domain of hIgG, followed by

either the c-jun or the c-fos leucine zippers described above [Kostelny, et al., J. Immunol. 148: 1547-1553 (1992)]. Since these leucine zippers form predominately heterodimers, they may be used to drive formation of the heterodimers where desired. As for the chimeric proteins described using leucine zippers, these may also be tagged with metal chelates or an epitope. This tagged domain can be used for rapid purification by metal-chelate chromatography, and/or by antibodies, to allow for detection on western blots, immunoprecipitation, or activity depletion/blocking in bioassays.

In additional embodiments, heterodimers may be prepared using other immunoglobulin derived domains that drive the formation of dimers. Such domains include, for example, the heavy chains of IgG (Cγ1 and Cγ4), as well as the constant regions of kappa (κ) and lambda (λ) light chains of human immunoglobulins. The heterodimerization of Cγ with the light chain occurs between the CH1 domain of Cγ and the constant region of the light chain (CL), and is stabilized by covalent linking of the two domains via a single disulfide bridge. Accordingly, as described in Example 4, constructs may be prepared using these immunoglobulin domains. Alternatively, the immunoglobulin domains include domains that may be derived from T cell receptor components which drive dimerization. In another embodiment of the invention, the sRα:β1 heterodimers are prepared by expression as chimeric molecules utilizing flexible linker loops. A DNA construct encoding the chimeric protein is designed such that it expresses two soluble or extracellular domains fused together in tandem ("head to head") by a flexible loop. This loop may be entirely artificial (e.g. polyglycine repeats interrupted by serine or threonine at a certain interval) or "borrowed" from naturally occurring proteins (e.g. the hinge region of hIgG). Molecules may be engineered in which the order of the soluble or extracellular domains fused is switched (e.g. sIL6Rα/loop/sgp130 or sgp130/loop/sIL-6Rα) and/or in which the length

and composition of the loop is varied, to allow for selection of molecules with desired characteristics.

Alternatively, the heterodimers made according to the present invention may be purified from cell lines cotransfected with the appropriate α and β components. Heterodimers may be separated from homodimers using methods available to those skilled in the art. For example, limited quantities of heterodimers may be recovered by passive elution from preparative, nondenaturing polyacrylamide gels. Alternatively, heterodimers may be purified using high pressure cation exchange chromatography. Excellent purification has been obtained using a Mono S cation exchange column.

In addition to sRα:β1 heterodimers that act as antagonists by binding free CNTF or IL-6, the present invention also contemplates the use of engineered, mutated versions of IL-6 with novel properties that allow it to bind to IL-6Rα and a single gp130 molecule, but fail to engage the second gp130 to complete β component homodimerization, and thus act as an effective IL-6 antagonist on any IL-6 responsive cell. Our model for the structure of the IL-6 and CNTF receptor complexes indicates that these cytokines have distinct sites for binding the α, β1, and β2 receptor components [Stahl and Yancopoulos, Cell 74: 587-590 (1993)]. Mutations of critical amino acid residues comprising each of these sites gives rise to novel molecules which have the desired antagonistic properties. Ablation of the β1 site would give a molecule which could still bind to the α receptor component but not the β1 component, and thereby comprise an antagonist with nanomolar affinity. Mutations of critical amino acid residues comprising the β2 site of IL-6 (IL-6β2$^-$) would give a molecule that would bind to IL-6Rα and the first gp130 monomer, but fail to engage the second gp130 and thus be functionally inactive. Similarly, mutations of

the CNTF β2 site would give a molecule (CNTFβ2-) that would bind CNTFRα and gp130, but fail to engage LIFRβ, thereby antagonizing CNTF action by forming the non-functional β1 intermediate. Based on the binding results described above where CNTF forms the β1 intermediate with high affinity, both CNTFβ2- and IL-6β2- would constitute antagonists with affinity in the range of 10 pM.

A variety of means are used to generate and identify mutations of IL-6 or CNTF that have the desired properties. Random mutagenesis by standard methods of the DNA encoding IL-6 or CNTF may be used, followed by analysis of the collection of products to identify mutated cytokines having the desired novel properties as outlined below. Mutagenesis by genetic engineering has been used extensively in order to elucidate the structural organization of functional domains of recombinant proteins. Several different approaches have been described in the literature for carrying out deletion or substitution mutagenesis. The most successful appear to be alanine scanning mutagenesis [Cunningham and Wells (1989), Science 244: 1081-1085] and homolog-scanning mutagenesis [Cunningham, et al., (1989), Science 243:1330-1336].

Targeted mutagenesis of the IL-6 or CNTF nucleic acid sequences using such methods can be used to generate CNTFβ2- or IL-6β2- candidates. The choice of regions appropriate for targeted mutagenesis is done systematically, or determined from studies whereby panels of monoclonal antibodies against each factor are used to map regions of the cytokine that might be exposed after binding of the cytokine to the α receptor component alone, or to the αβ1 heterodimeric soluble receptors described above. Similarly, chemical modification or limited proteolysis of the cytokine alone or in a complex bound to the α receptor component or the αβ1 heterodimeric soluble receptors described above, followed by analysis

of the protected and exposed regions could reveal potential β2 binding sites.

Assays for identifying CNTF or IL-6 mutants with the desired properties involve the ability to block with high affinity the action of IL-6 or CNTF on appropriately responsive cell lines [Davis, et al., Science 259: 1736-1739 (1993); Murakami, et al., Proc. Natl. Acad. Sci. USA 88: 11349-11353 (1991)]. Such assays include cell proliferation, survival, or DNA synthesis driven by CNTF or IL-6, or the construction of cell lines where binding of factor induces production of reporters such as CAT or β–galactosidase [Savino, et al., Proc. Natl. Acad. Sci. USA 90: 4067-4071 (1993)].

Alternatively, the properties of various mutants may be assessed with a receptor-based assay. One such assay consists of screening mutants for their ability to bind the sRα:β1 receptor heterodimers described above using epitope-tagged [Davis et al., Science 253: 59-63 (1991)] sRα:β1 reagents. Furthermore, one can probe for the presence or absence of the β2 site by assessing whether an epitope-tagged soluble β2 reagent will bind to the cytokine in the presence of the β1 heterodimer. For example, CNTF only binds to LIFRβ (the β2 component) in the presence of both CNTFRα and gp130 [Davis, et al. Science 260: 1805-1808 (1993); Stahl, et al. J. Biol. Chem. 268: 7628-7631 (1993)]. Thus a soluble LIFRβ reagent would only bind to CNTF in the presence of the soluble sRα:β1 dimer sCNTFRα:β1. For IL-6, the sRα:β1 reagent would be IL-6Rα:β1, and the probe for the β2 site would be epitope-tagged sgp130. Thus $\beta 2^-$ mutants of CNTF would be identified as those that bound the sRα:β1 reagent, demonstrating that the α and β1 site of the cytokine were intact, yet failed to bind the β2 reagent.

In addition, the present invention provides for methods of detecting or measuring the activity of potential β2- mutants by measuring the phosphorylation of a β-receptor component or a signal transduction component selected from the group consisting of Jak1, Jak2 and Tyk2 or any other signal transduction component, such as the CLIPs, that are determined to be phosphorylated in response to a member of the CNTF family of cytokines.

A cell that expresses the signal transduction component(s) described herein may either do so naturally or be genetically engineered to do so. For example, Jak1 and Tyk-2-encoding nucleic acid sequences obtained as described in Velazquez, et al., Cell, Vol. 70:313-322 (1992), may be introduced into a cell by transduction, transfection, microinjection, electroporation, via a transgenic animal, etc., using any known method known in the art.

According to the invention, cells are exposed to a potential antagonist and the tyrosine phosphorylation of either the β-component(s) or the signal transduction component(s) are compared to the tyrosine phosphorylation of the same component(s) in the absence of the potential antagonist. In another embodiment of the invention, the tyrosine phosphorylation that results from contacting the above cells with the potential antagonist is compared to the tyrosine phosphorylation of the same cells exposed to the parental CNTF family member. In such assays, the cell must either express the extracellular receptor (α-component) or the cells may be exposed to the test agent in the presence of the soluble receptor component. Thus, for example, in an assay system designed to identify agonists or antagonists of CNTF, the cell may express the α- component CNTFRα, the β-components gp130 and LIFRβ and a signal transducing component such as Jak1. The cell is exposed to test agents, and the tyrosine phosphorylation of either the β- components or the signal transducing component is

compared to the phosphorylation pattern produced in the presence of CNTF. Alternatively, the tyrosine phosphorylation which results from exposure to a test agent is compared to the phosphorylation which occurs in the absence of the test agent. Alternatively, an assay system, for example, for IL-6 may involve exposing a cell that expresses the β-component gp130 and a signal transducing protein such as Jak1, Jak2 or Tyk2 to a test agent in conjunction with the soluble IL-6 receptor.

In another embodiment of the invention the above approaches are used to develop a method for screening for small molecule antagonists that act at various steps in the process of ligand binding, receptor complex formation, and subsequent signal transduction. Molecules that potentially interfere with ligand-receptor interactions are screened by assessing interference of complex formation between the soluble receptors and ligand as described above. Alternatively, cell-based assays in which IL-6 or CNTF induce response of a reporter gene are screened against libraries of small molecules or natural products to identify potential antagonists. Those molecules showing antagonist activity are rescreened on cell-based assays responding to other factors (such as GM-CSF or factors like Neurotrophin-3 that activate receptor tyrosine kinases) to evaluate their specificity against the CNTF/IL-6/OSM/LIF family of factors. Such cell-based screens are used to identify antagonists that inhibit any of numerous targets in the signal transduction process.

In one such assay system, the specific target for antagonists is the interaction of the Jak/Tyk family of kinases [Firmbach-Kraft, Oncogene 5: 1329-1336 (1990); Wilks, et al., Mol. Cell. Biol. 11:2057-2065 (1991)] with the receptor β subunits. As described above, LIFRβ and gp130 preassociate with members of the Jak/Tyk family of cytoplasmic protein tyrosine kinases, which become activated in response to ligand-induced β component dimerization Stahl, et al. Science 263:92-95 (1993). Thus small molecules that could enter the cell cytoplasm and disrupt the interaction

between the β component and the Jak/Tyk kinase could potentially block all subsequent intracellular signaling. Such activity could be screened with an *in vitro* scheme that assessed the ability of small molecules to block the interaction between the relevant binding domains of purified β component and Jak/Tyk kinase. Alternatively, one could easily screen for molecules that could inhibit a yeast-based assay of β component binding to Jak/Tyk kinases using the two-hybrid interaction system [Chien, et al., Proc. Natl. Acad. Sci. 88: 9578-9582 (1991)]. In such a system, the interaction between two proteins (β component and Jak/Tyk kinase or relevant domains thereof in this example) induces production of a convenient marker such as β- galactosidase. Collections of small molecules are tested for their ability to disrupt the desired interaction without inhibiting the interaction between two control proteins. The advantage of this screen would be the requirement that the test compounds enter the cell before inhibiting the interaction between the β component and the Jak/Tyk kinase.

The CNTF family antagonists described herein either bind to, or compete with the cytokines CNTF and IL-6. Accordingly, they are useful for treating diseases or disorders mediated by CNTF or IL-6. For example, therapeutic uses of IL-6 antagonists would include the following:

1) In osteoporosis, which can be exacerbated by lowering of estrogen levels in post-menopausal women or through ovariectomy, IL-6 appears to be a critical mediator of osteoclastogenesis, leading to bone resorption [Horowitz, Science 260: 626-627 (1993); Jilka, et al., Science 257: 88-91 (1992)]. Importantly, IL-6 only appears to play a major role in the estrogen-depleted state, and apparently is minimally involved in normal bone maintenance. Consistent with this, experimental evidence indicates that function-blocking antibodies to IL-6 can reduce the number of osteoclasts [Jilka, et al. Science 257: 88-91 (1992)]. While estrogen replacement therapy is also used, there appear to be side effects that may include increased risk of

endometrial and breast cancer. Thus, IL-6 antagonists as described herein would be more specific to reduce osteoclastogenesis to normal levels.

2) IL-6 appears to be directly involved in multiple myeloma by acting in either an autocrine or paracrine fashion to promote tumor formation [van Oers, et al., Ann Hematol. 66: 219-223 (1993)]. Furthermore, the elevated IL-6 levels create undesirable secondary effects such as bone resorption, hypercalcemia, and cachexia; in limited studies function-blocking antibodies to IL-6 or IL-6Ra have some efficacy [Klein, et al., Blood 78: 1198-1204 (1991); Suzuki, et al., Eur. J. Immunol. 22:1989-1993 (1992)]. Therefore, IL-6 antagonists as described herein would be beneficial for both the secondary effects as well as for inhibiting tumor growth.

3) IL-6 may be a mediator of tumor necrosis factor (TNF) that leads to cachexia associated with AIDS and cancer [Strassmann, et al., J. Clin. Invest. 89: 1681-1684 (1992)], perhaps by reducing lipoprotein lipase activity in adipose tissue [Greenberg, et al., Cancer Research 52: 4113-4116 (1992)]. Accordingly, antagonists described herein would be useful in alleviating or reducing cachexia in such patients.

Effective doses useful for treating these or other CNTF family related diseases or disorders may be determined using methods known to one skilled in the art [see, for example, Fingl, et al., The Pharmacological Basis of Therapeutics, Goodman and Gilman, eds. Macmillan Publishing Co., New York, pp. 1-46 ((1975)]. Pharmaceutical compositions for use according to the invention include the antagonists described above in a pharmacologically acceptable liquid, solid or semi-solid carrier, linked to a carrier or targeting molecule (e.g., antibody, hormone, growth factor, etc.) and/or incorporated into liposomes, microcapsules, and controlled release preparation (including antagonist expressing cells) prior to administration *in vivo*. For example, the pharmaceutical composition may comprise one or more of the antagonists in an aqueous solution, such as sterile water, saline, phosphate buffer or dextrose solution. Alternatively, the active agents may be comprised in a solid (e.g. wax) or semi-solid (e.g. gelatinous) formulation that may be implanted into a patient in need of such

treatment. The administration route may be any mode of administration known in the art, including but not limited to intravenously, intrathecally, subcutaneously, by injection into involved tissue, intraarterially, intranasally, orally, or via an implanted device.

Administration may result in the distribution of the active agent of the invention throughout the body or in a localized area. For example, in some conditions which involve distant regions of the nervous system, intravenous or intrathecal administration of agent may be desirable. In some situations, an implant containing active agent may be placed in or near the lesioned area. Suitable implants include, but are not limited to, gelfoam, wax, or microparticle-based implants.

EXAMPLES

EXAMPLE 1: CNTF COMPETES WITH IL-6 FOR BINDING TO GP130

MATERIALS AND METHODS

Materials. A clone of PC12 cells that respond to IL-6 (PC12D) was obtained from DNAX. Rat CNTF was prepared as described [Masiakowski, et al., J. Neurochem. 57:1003-10012 (1991)]. IL-6 and sIL-6Rα were purchased from R & D Systems. Antisera was raised in rabbits against a peptide derived from a region near the C-terminus of gp130 (sequence: CGTEGQVERFETVGME) [SEQ. ID. NO. 2] by the method described (Stahl, et al. J. Biol. Chem. 268:7628-7631 (1993). Anti-phosphotyrosine monoclonal 4G10 was purchased from UBI, and reagents for ECL from Amersham.

Signal Transduction Assays. Plates (10 cm) of PC12D were starved in serum-free medium (RPMI 1640 + glutamine) for 1 hour, then incubated with IL-6 (50 ng/mL) + sIL-6R (1 mg/mL) in the presence or absence of

added rat CNTF at the indicated concentrations for 5 minutes at 37°C. Samples were then subjected to anti-gp130 immunoprecipitation, SDS PAGE, and anti-phosphotyrosine immunoblotting as described (Stahl, et al. J. Biol. Chem. 268:7628-7631 (1993).

RESULTS

The ability of CNTF to block IL-6 responses was measured using a PC12 cell line (called PC12D) that expresses IL-6Rα, gp130, and CNTFRα, but not LIFRβ. As one would predict, these cells respond to IL-6, but not to CNTF (Fig. 2) since LIFRβ is a required component for CNTF signal transduction [Davis, et al., Science 260: 59-63 (1993)]. In accordance with results on other cell lines [Ip, et al., Cell 69: 1121-1132 (1992)], PC12D cells give tyrosine phosphorylation of gp130 (as well as a variety of other proteins called CLIPs) in response to 2 nM IL-6 (Fig. 2). Addition of recombinant soluble IL-6Rα (sIL-6Rα) enhances the level of gp130 tyrosine phosphorylation, as has been reported in some other systems [(Taga, et al., Cell 58: 573-581 (1989)]. However, addition of 2 nM CNTF simultaneously with IL-6 severely diminishes the tyrosine phosphorylation of gp130. Although a slight gp130 phosphorylation response remains in the presence of CNTF, IL-6, and sIL-6Rα, it is eliminated if the CNTF concentration is increased fourfold to 8 nM. Thus, in IL-6 responsive cells that contain CNTFRα but no LIFRβ, CNTF is a rather potent antagonist of IL-6 action.

EXAMPLE 2. BINDING OF CNTF TO THE CNTFRα:β

MATERIALS AND METHODS

Scatchard Analysis of CNTF Binding. ^{125}I-CNTF was prepared and purified as described [Stahl et al. JBC 268: 7628-7631 (1993)]. Saturation binding studies were carried out in PC12 cells, using concentrations of ^{125}I-

CNTF ranging from 20pM to 10nM. Binding was performed directly on a monolayer of cells. Medium was removed from wells and cells were washed once with assay buffer consisting of phosphate buffered saline (PBS; pH 7.4), 0.1mM bacitracin, 1mM PMSF, 1mg/ml leupeptin, and 1mg/ml BSA. Cells were incubated in ^{125}I-CNTF for 2 hours at room temperature, followed by 2 quick washes with assay buffer. Cells were lysed with PBS containing 1% SDS and counted in a Packard Gamma Counter at 90-95% efficiency. Non-specific binding was defined by the presence of 100-fold excess of unlabelled CNTF. Specific binding ranged from 70% to 95%.

RESULTS

The equilibrium constant for binding of CNTF to CNTFRα:β1 was estimated from Scatchard analysis of iodinated CNTF binding on PC12D cells (Figure 3). The data is consistent with a 2 site fit having dissociation constants of 9 pM and 3.4 nM. The low affinity site corresponds to interaction of CNTF with CNTFRα , which has a Kd near 3 nM [(Panayotatos, et al., J. Biol. Chem. 268: 19000-19003 (1993)]. We interpret the high affinity complex as the intermediate containing CNTF, CNTFRα , and gp130. A Ewing sarcoma cell line (EW-1) which does contain CNTFRα, gp130, and LIFRβ, and therefore gives robust tyrosine phosphorylation in response to CNTF, displays a very similar two site fit with dissociation constants of 1 nM and 10. Thus it is apparent that CNTF binds with equally high affinity to a complex containing only CNTFRα and gp130, as it does to a complex which additionally contains LIFRβ, thus demonstrating the feasibility of creating the sRα:β antagonists described herein.

EXAMPLE 3. METHODS OF PRODUCING CYTOKINE LIGAND TRAPS

Virus Stock Production

SF21 insect cells obtained from *Spodoptera frugiperda* were grown at 27°C in Gibco SF900 II medium to a density of $1x10^6$ cells/mL. The individual virus stock for either GP130-Fc-His_6 (Figure 4) or IL6Ra-Fc (Figure 5) was added to the bioreactor to a low multiplicity 0.01-0.1 PFU/cell to begin the infection. The infection process was allowed to continue for 5-7 days allowing maximum virus replication without incurring substantial cell lysis. The cell suspension was aseptically aliquoted into sterile centrifuge bottles and the cells removed by centrifugation. The cell-free supernatant was collected in sterile bottles and stored at 4°C until further use.

The virus titer was determined by plaque assay as described by O'Reilly, Miller and Luckow. The method is carried out in 60mm tissue-culture dishes which are seeded with $2x10^6$ cells. Serial dilutions of the virus stock are added to the attached cells and the mixture incubated with rocking to allow the virus to adsorb to individual cells. An agar overlay is added and plates incubated for 5 - 7 days at 27°C. Staining of viable cells with neutral red revealed circular plaques resulting which were counted to give the virus titer.

Coinfection of Cells for Protein Production

Uninfected SF21 Cells were grown in a 60L ABEC bioreactor containing 40L of SF900 II medium. Temperature was controlled at 27°C and the dissolved oxygen level was maintained at 50% of saturation by controlling the flowrate of oxygen in the inlet gas stream. When a density of $2x10^6$ cells/mL was reached, the cells were concentrated within the bioreactor to a volume of 20L using a low shear steam sterilizable pump with a tangential flow filtration device with Millipore Prostak 0.65 micron

membranes. After concentration fresh sterile growth medium is slowly added to the bioreactor while the filtration system continues to remove the spent growth medium by diafiltration. After two volume exchanges (40L) have been carried out an additional 20L of fresh medium was added to the bioreactor to resuspend the cells to the original volume of 40L. The cell density was determined once again by counting viable cells using a hemacytometer.

The required amount of each virus stock was calculated based on the cell density, virus titer and the desired multiplicity of infection (MOI). Virus stock ratios of 5:1, 5:2, 10:2 and 10:4, IL6Rα-Fc to GP130-Fc-His_6 all resulted in production of significant amounts of heterodimer. The ideal virus stock ratio is highly dependent on the ease of purification of the heterodimer from each of the two homodimers. The IL6Rα-Fc homodimer is relatively easy to remove downstream by immobilized metal affinity chromatography. Virus infection ratios have been chosen to minimize the formation of the GP130-Fc-His_6 homodimer which is more difficult to clear downstream. The relative amount of GP130-Fc-His_6 virus stock chosen for infection has increased with successive batches as the purification method for clearing the resultant homodimer has improved.

The virus stocks were aseptically mixed in a single vessel then transferred to the bioreactor. This results in synchronous infection of the SF21 cells. The infection is allowed to proceed for three to four days, allowing sufficient time for maximal production of the heterodimer protein.

Recovery and Protein A Chromatographic Purification

At the conclusion of the infection phase of the bioreactor process the cells were concentrated in the bioreactor using a 10 ft^2 Millipore Prostak filter (0.65 micron) pore size. The cell-free permeate passing through the filter was collected in a clean process vessel. At the conclusion of the filtration

operation the pH of permeate stream, containing the protein product, was adjusted to 8.0 with 10N NaOH. The resultant precipitate was removed by forcing the extract through a 0.8 micron depth filter (Sartorious), followed by a 0.2 micron filter. Sufficient 0.5M EDTA stock was added to give a final concentration of 5mM. The filtered protein solution was loaded onto a 10 cm diameter column containing 100-200 mL of Pharmacia Protein A Sepharose 4 Fast Flow, equilibrated with PBS. Protein A has a very high affinity for the Fc-Fc domain of each of the 3 recombinant protein products, allowing them to bind while other proteins in the cell-free extract flow through the column. After loading the column was washed to baseline with PBS containing an additional 350mM NaCl. The IgG-Fc tagged proteins were eluted at low pH, either with 0.5M acetic acid or with a decreasing pH gradient of 0.1M citric acid and 0.2M disodium phosphate buffers. Tris base or disodium phosphate was added to the eluted protein to avoid prolonged exposure to low pH conditions.

The pooled protein was diafiltered into PBS or HEPES buffer and derivitized with 1 mM iodoacetamide to protect the exposed sulfhydryl group on the free cysteine near the hinge region of each Fc domain. This prevents disulfide mediated aggregation of proteins. A 6 ft^2 Millipore spiral wound ultrafiltration membrane with nominal 30 kiloDalton cutoff was used to perform the buffer exchange. The total protein was determined by UV absorbance at 280 nm using the diafiltration buffer as a blank. The relative amounts of heterodimer and two homodimer proteins were determined by SDS PAGE gel electrophoresis using a 6% Tris-Glycine gel (Novex). Gels were Coomassie-stained then transferred into destain solution overnight. A Shimadzu scanning densitometer was used to determine the relative intensity of the individual protein bands on the SDS PAGE gel. The peak area ratios are used to compute the fraction of heterodimer and each of the homodimers in the column pool fractions.

Immobilized Metal Affinity Chromatographic Purification

The six histidine residues on the C-terminus of the GP130-Fc-His_6 fusion protein provides an excellent molecular handle for separation of the heterodimeric IL6 antagonist from the two homodimers. The imidazole group on each of the C-terminal histidines of the GP130-Fc-His_6 moiety has a strong binding constant with several divalent metals, including copper, nickel, zinc, cobalt, iron and calcium. Since the IL6Rα-Fc homodimer has no C-terminal histidine residues, it clearly has the lowest affinity. The IL6Rα-Fc-GP130-Fc-His_6 heterodimer has a single stand set six histidines giving it greater affinity for the metal, while the GP130-Fc-His_6 homodimer has two sets of six histidines each giving it the highest affinity of the three IgG tagged proteins to the metal affinity column. Selective elution of the three proteins with increasing amounts of imidazole in the elution buffer therefore elutes the proteins in the following order:

1. IL6Rα-Fc homodimer
2. IL6Rα-Fc-GP130-Fc-His heterodimer
3. GP130-Fc-His homodimer

A 26 mm diameter column containing 100 mL of Pharmacia Chelating Sepharose Fast Flow was saturated with a solution of nickel sulfate until a significant green color is observed in the column eluate. The column is then washed with several column volumes of deionized water, then equilibrated with 50 mM HEPES, 40mM imidazole, pH 8.0. The binding of imidazole to the immobilized nickel results in a green to blue color change. Imidazole was added to the protein load to a final concentration of 40mM. Addition of imidazole to the protein load reduces the binding of IL6Rα-Fc homodimer, increasing the surface area available for the remaining two species. After loading, the column was washed with

several column volumes of 50 mM HEPES, 80mM imidazole, pH 8.0 until a steady baseline was reestablished. The heterodimer was selectively eluted with 50 mM HEPES, 150mM imidazole, pH 8.0 over several column volumes. The protein fractions were pooled and diafiltered into PBS as described in the section above.

EXAMPLE 4. ALTERNATIVE METHODS OF CONSTRUCTING LIGAND TRAPS

As described above, receptor activation by CNTF, and analogously by IL-6 and IL-11, follows an ordered sequence of binding events (Figure 6). The cytokine initially binds to its cognate Rα with low affinity (Kd = 3 to 10 nM); this is a required step - cells which do not express the cognate Rα do not respond to the cognate cytokine. The cytokine•Rα complex associates with the first signal transducing component, gp130, to form a high affinity complex (Kd in the order of 10 pM for the CNTF•CNTFRα•gp130 complex). This complex does not transduce signal, as it is the dimerization of the signal transducing components that brings about signaling (Stahl and Yancopoulos, J. Neurobiology 25: 1454-1466 (1994); Stahl et al., Science 267:1349-1353 (1995); Davis et al., Science 260:1805-1808 (1993); Stahl et al., Science 263:92-95 (1994); Murakami, et al. Science 260:1808-1810 (1993). At least in the case of IL-6, the cytokine•Rα•signal transducer heterotrimeric complex subsequently associates with another like complex, to form a hexameric complex (Figure 6) (Ward et al., J. Biol. Chem. 269:23286-23289 (1994). The resulting dimerization of the signal transducers - gp130 in the case of IL-6 (Murakami et al., Science 260:1808-1810 (1993) and IL-11, gp130 and LIFR in the case of CNTF (Davis et al., Science 260:1805-1808 (1993) - brings about signal transduction.

The initial heterodimeric molecules made comprised a soluble Rα-component linked to the extracellular domain of gp130. These molecules

were shown to mimic the high affinity cytokine•Rα•gp130 complex and behave as a high affinity antagonist of their cognate cytokine (Figure 7). To make these molecules, the extracellular domain of gp130 was paired with the extracellular domain of the α-receptor components for IL-6 and CNTF, IL-6Rα and CNTFRα respectively. To link the Rα with the extracellular domain of gp130, the soluble Rα-components and gp130 were fused to the Fc portion of human IgG1 to produce Rα-Fc and gp130-Fc respectively. The Fc domain was chosen primarily but not solely because it naturally forms disulfide-linked dimers. Heterodimeric molecules comprising Rα–Fc•gp130-Fc were expressed, purified and shown to behave as highly potent antagonists of their cognate ligand. Furthermore, these molecules were found to be highly specific for their cognate cytokine since it is the choice of the α–receptor component which specifies which cytokine is bound and trapped (there is no measurable binding of the cytokine to gp130 in the absence of the appropriate Rα).

Here we describe an extension of this technology which allows the engineering of different heteromeric soluble receptor ligand traps which by virtue of their design may have additional beneficial characteristics such as stability, Fc-receptor-mediated clearance, or reduced effector functions (such as complement fixation). Furthermore, the technology described should prove suitable for the engineering of any heteromeric protein in mammalian or other suitable protein expression systems, including but not limited to heteromeric molecules which employ receptors, ligands, and catalytic components such as enzymes or catalytic antibodies.

MATERIALS AND METHODS

Genetic engineering of heteromeric immunoglobulin heavy/light chain soluble receptor-based ligand traps for IL-6.

The IL-6 traps described here were engineered using human gp130, human IL-6 α-receptor (IL-6Rα), the constant region of the heavy chains (Cγ) of human IgG1 (**Cγ1**) (Lewis et al., Journal of Immunology 151:2829-2838 (1993) or IgG4 (**Cγ4**) with or without a join-region (**J**), and the constant regions of kappa (κ) and lambda (λ) (Cheung, et al., Journal of Virology 66:6714-6720 (1992) light chains of human immunoglobulin (**Ig**), also with or without a different j-peptide (**j**). This design takes advantage of the natural ability of the Cγ domain to heterodimerize with κ or λ light chains. The heterodimerization of Cγ with the light chain occurs between the CH1 domain of Cγ and the constant region of the light chain (C_L), and is stabilized by covalent linking of the two domains via a single disulfide bridge. We reasoned that, like the Fc domain of human IgG1, the combination of Cγ with C_L could be used to produce disulfide linked heteromeric proteins comprised of the extracellular domain of gp130 on one chain and the extracellular domain of IL-6Rα on the other chain. Like their Fc-based counterparts, such proteins were postulated to be high affinity ligand traps for IL-6 and as a result to inhibit the interaction of IL-6 with the native receptor on IL-6-responsive cells, thus functioning as IL-6 antagonists. Furthermore, constructs employing the full length Cγ region would, much like antibodies, form homodimers of the Cγ chain, giving rise to antibody-like molecules comprising of two "light chains" and two "heavy chains" (Figure 8). The potential advantage of this design is that it may more closely mimic the IL-6•IL-6Rα•gp130 complex and may display a higher affinity for the ligand than comparable single heterodimers. An additional design is incorporated by using truncated versions of Cγ, comprised only of the C_H1 domain. These will form heterodimeric molecules with receptor-κ fusion proteins, and will thus resemble the Fab fragment of antibodies.

All the soluble receptor-Ig chimeric genes may be engineered in plasmid vectors including, but not limited to, vectors suitable for mammalian expression (COS monkey kidney cells, Chinese Hamster Ovary cells [CHO], and ras-transformed fibroblasts [MG-ras]) and include a Kozak sequence (CGC CGC CAC CAT GGT G) at the beginning of each chimeric gene for efficient translation. Engineering was performed using standard genetic engineering methodology. Each construct was verified by DNA sequencing, mammalian expression followed by western blotting with suitable antibodies, biophysical assays that determine ligand binding and dissociation, and by growth inhibition assays (XG-1, as described later). Since the domains utilized to engineer these chimeric proteins are flanked by appropriate restriction sites, it is possible to use these domains to engineer other chimeric proteins, including chimeras employing the extracellular domains of the receptors for factors such as IL-1, IL-2, IL-3, IL-4, IL-5, GM-CSF, LIF, IL-11, IL-15, IFNγ, TGFβ, and others. The amino acid coordinates for each component utilized in making the IL-6 traps are listed below (Note: numbering starts with the initiating methionine as #1; long sequences are listed using the single letter code for the twenty amino acids):

(a) Constructs employing human gp130:

(i) **gp130-Cγ1** was engineered by fusing in frame the extracellular domain of gp130 (amino acids 1 to 619) to a Ser-Gly bridge, followed by the 330 amino acids which comprise Cγ1 and a termination codon (Figure 9).

(ii) **gp130-J-Cγ1** was engineered in the same manner as gp130-Cγ1 except that a J-peptide (amino acid sequence: GQGTLVTVSS) was inserted between the Ser-Gly bridge and the sequence of Cγ1 (see Figure 9).

(iii) **gp130Δ3fibro-Cγ1** was engineered by fusing in frame the extracellular domain of gp130 without its three fibronectin-like domains (Figure 10). The remaining part of this chimeric protein is identical to gp130-Cγ1.

(iv) **gp130-J-C_H1** was engineered in a manner identical for that described for gp130-Cγ1, except that in place of the Cγ1 region only the C_H1 part of Cγ1 has been used (Figure 11). The C-terminal domain of this construct includes the part of the hinge that contains the cysteine residue responsible for heterodimerization of the heavy chain of IgG with a light chain. The part of the hinge that contains the two cysteines involved in Cγ1 homodimerization has been deleted along with the C_H2 and C_H3 domains.

(v) **gp130-Cγ4** was engineered in a manner identical to that described for gp130-Cγ1, except that Cγ4 was used in place of Cγ1 (Figure 12). In addition, an *Rsr*II DNA restriction site was engineered at the hinge region of the Cγ4 domain by introducing two silent base mutations. The *Rsrs*II site allows for other desired genetic engineering manipulations, such as the construction of the C_H1 equivalent of gp130-Cγ4.

(vi) **gp130-κ** was engineered in a manner identical to that described for gp130-Cγ1, except that the constant region of the κ light chain of human Ig was used in place of Cγ1 (Figure 13).

(vi) **gp130-J-κ** was engineered in a manner identical to that described for gp130-J-κ, except that a j-peptide (amino acid sequence: TFGQGTKVEIK) was inserted between the Ser-Gly bridge and the κ-region.

(viii) **gp130-λ** was engineered in a manner identical to that described for gp130-Cγ1, except that the constant region of the λ light chain (Cheung, et al., Journal of Virology 66:6714-6720 (1992) of human Ig was used in place of Cγ1 (Figure 14).

(b) Constructs employing human IL-6Rα:

(i) **IL6Rα-Cγ1** was engineered by fusing in frame amino acids 1 to 358 of IL-6Rα (Yamasaki et al., Science 241:825-828 (1988), which comprise the

extracellular domain of IL-6Rα (Figure 15), to an Ala-Gly bridge, followed by the 330 amino acids which comprise Cγ1 and a termination codon.

(ii) **IL6Rα-κ** was engineered as described for IL6Rα-Cγ1, except that the κ-domain (Figure 13) utilized for gp130-κ was used in place of Cγ1.

(iii) **IL6Rα-j-κ** was engineered as described for IL6Rα-κ except that the j-peptide described for gp130-j-κ was placed between the Ala-Gly bridge and the κ-domain.

(iv) Three additional constructs, **IL6Rα313-Cγ1**, **IL6Rα313-κ**, and **IL6Rα313-j-κ**, were engineered as using a truncated form of IL-6Rα comprised of amino acids 1 to 313 (Figure 16). Each of these constructs were made by fusing in frame IL6Rα313 with a Thr-Gly bridge followed by the Cγ1, κ-, and j-κ-domains described above. These constructs were engineered in order to complement the gp130Δ3fibro-derived constructs.

Expression and purification of ligand traps

To produce covalently linked heterodimers of soluble gp130 and soluble IL-6Rα, gp130-Ig chimeric proteins were co-expressed with appropriate IL-6Rα-Ig chimeric proteins in complementing pairs. Co-expression was achieved by co-transfecting the corresponding expression vectors into suitable mammalian cell lines, either stably or transiently. The resulting disulfide-linked heterodimers were purified from conditioned media by several different methods, including but not limited to affinity chromatography on immobilized Protein A or Protein G, ligand-based affinity chromatography, ion exchange, and gel filtration.

An example of the type of methods used for purification of a heavy/light receptor fusion protein is as follows: gp130-Cγ1•IL-6Rα-κ was expressed in COS cells by co-transfecting two different vectors, encoding gp130-Cγ1 and

IL-6Rα-κ respectively. Serum-free conditioned media (400 ml) were collected two days post-transfection and Cγ1-bearing proteins were purified by affinity chromatography over a 1ml Protein A Sepharose (Pharmacia). The material generated in this step was further purified by a second affinity chromatography step over a 1 ml NHS-activated Sepharose (Pharmacia) which was derivatized with recombinant human IL-6, in order to remove gp130-Cγ1 dimer from gp130-Cγ1•IL-6Rα-κ complexes (the gp130-Cγ1 dimer does not bind IL-6). Proteins generated by this method were more than 90% pure, as evidenced by SDS-PAGE followed by silver-staining (Figure 17). Similar protocols have been employed successfully towards the purification of other heavy/light receptor heterodimers.

RESULTS

Biological activity of immunoglobulin heavy/light chain receptor fusion antagonists

The purified ligand traps were tested for their ability to bind IL-6 in a variety of different assays. For example, the dissociation rate of IL-6 bound to the ligand trap was measured in parallel with the dissociation rate of IL-6 from the anti-IL-6 monoclonal neutralizing antibody B-E8 [Brochier, et al., Int. J. Immunopharmacology 17:41-48 (1995), and references within]. An example of this type of experiment is shown in Figure 18. In this experiment 20 pM ^{125}I-IL-6 (1000 μCi/mmol; Amersham) was preincubated with 500 pM of either gp130-Cγ1•IL-6Rα-κ or mAb B-E8 for 20 hours. At this point a 1000-fold excess (20 nM) of "cold" IL-6 was added. Periodically, aliquots of the reaction were removed, the ligand trap or B-E8 were precipitated with Protein G-Sepharose, and the number of cpm of ^{125}I-IL-6 that remained bound was determined. Clearly, the dissociation rate of human ^{125}I-IL6 from the ligand trap was very slow - after three days, approximately 75% of the initial counts were still bound to the ligand

trap. In contrast, less than 5% of the counts remained associated with the antibody after three days. This result demonstrates that the dissociation rate of the ligand from these ligand traps is very slow.

In a different set of experiments the ability of the ligand traps to multimerize in the presence of ligand was tested. An example of this is shown in Figure 19. IL-6-induced association of gp130-Fc•IL-6Rα-Fc with gp130-C_H1•IL-6Rα-κ was determined by testing whether gp130-C_H1•IL-6Rα-κ, which does not by itself bind Protein A, could be precipitated by Protein A-Sepharose in the presence of gp130-Fc•IL-6Rα-Fc in an IL-6-depended manner (Figure 9). Precipitation of gp130-C_H1•IL-6Rα-κ by Protein A-Sepharose was determined by western blotting with an anti-kappa specific HRP conjugate, which does not detect gp130-Fc•IL-6Rα-Fc. gp130-C_H1•IL-6Rα-κ could be precipitated by Protein A-Sepharose only when both gp130-Fc•IL-6Rα-Fc and IL-6 were present. This result conclusively indicates that IL-6 can induce ligand trap multimerization, and further indicate that the ligand trap can mimic the hexameric cytokine•Rα•signal transducer complex (Figure 1). Ligand-induced multimerization may play a significant role in the clearance of cytokine•ligand trap complexes *in vivo*.

The biological activity of the different ligand traps may be further tested in assays which measure ligand-depended cell proliferation. Several cell proliferation assays exist for IL-6 and they employ cell lines such as B9, CESS, or XG-1. An example of this type of assay using the XG-1 cell line is presented below: XG-1 is a cell line derived from a human multiple myeloma (Zhang, et al., Blood 83:3654-3663 (1994). XG-1 depends on exogenously supplied human IL-6 for survival and proliferation. The EC_{50} of IL-6 for the XG-1 line is approximately 50 pmoles/ml. The ability of several different IL-6 traps to block IL-6-depended proliferation of XG-1

cells was tested by incubating increasing amounts of purified ligand traps with 50 pg/ml IL-6 in XG-1 cultures. The ligand traps which were tested had been expressed and purified by methods similar to those described above. All of the ligand traps tested were found to inhibit IL-6-dependent proliferation of XG-1 in a dose dependent manner (Figure 20). Of the five different traps tested gp130-Cγ1•IL-6Rα-κ was the most active and essentially display the same neutralizing activity towards IL-6 as the antibody B-E8. As little as a 10-fold molar excess of either gp130-Cγ1•IL-6Rα-κ or B-E8 completely blocked the activity of IL- 6 (a reading of A570-650 = 0.3 AU corresponds to no proliferation of the XG-1 cells). At a 100-fold molar excess all of the ligand traps tested completely blocked the activity of IL-6. This observed inhibition is highly selective as neither a gp130-Fc•CNTFRα-Fc ligand trap which blocks CNTF activity, nor gp130-Fc homodimer exhibit any blocking activity towards IL-6 even when used at a 1000-fold molar excess over IL-6 (data not shown). This data demonstrates that the heteromeric immunoglobulin heavy/light chain receptor-based ligand traps function as selective high affinity antagonists of their cognate ligand.

EXAMPLE 5 - CLONING OF FUSION POLYPEPTIDE COMPONENTS

The extracellular domains of the human cytokine receptors were obtained by standard PCR techniques using tissue cDNAs (CLONTECH), cloned into the expression vector, pMT21 (Genetics Institute, Inc.), and the sequences were sequenced by standard techniques using an ABI 373A DNA sequencer and Taq Dideoxy Terminator Cycle Sequencing Kit (Applied Biosystems, Inc., Foster City, CA). For the IL-4Rα, nucleotides 241 through 868 (corresponding to the amino acids 24-231) from the Genbank sequence, X52425, were cloned. For the IL-2Rγ, nucleotides 15 through 776 (corresponding to amino acids 1-233) from the Genbank sequence, D11086, were cloned. For the IL-6Rα, nucleotides 52 through 1044 (corresponding

to the amino acids 1-331) from the Genbank sequence, X52425, were cloned. For gp130, nucleotides 322 through 2112 (corresponding to the amino acids 30-619) from the Genbank sequence, M57230, were cloned. For the IL-1RAcP, nucleotides 1 through 1074 (corresponding to the amino acids 1-358) from the Genbank sequence, AB006357, were cloned. For the IL-1RI, nucleotides 55 through 999 (corresponding to the amino acids 19-333) from the Genbank sequence, X16896, were cloned.

EXAMPLE 6 - PRODUCTION OF FUSION POLYPEPTIDES (CYTOKINE TRAPS)

The nucleotide sequences encoding the cytokine traps were constructed from the individual cloned DNAs (described *supra*) by standard cloning and PCR techniques. In each case, the sequences were constructed in frame such that the sequence encoding the first fusion polypeptide component was fused to the sequence encoding the second fusion polypeptide component followed by an Fc domain (hinge, CH2 and CH3 region of human IgG1) as the multimerizing component. In some cases extra nucleotides were inserted in frame between sequences encoding the first and second fusion polypeptide components to add a linker region between the two components (See Figure 21A - Figure 21D - trap 424; Figure 24A - Figure 24F - trap 412; and Figure 26A - Figure 26E - trap 569).

For the IL-4 traps, 424 (Figure 21A - Figure 21D), 603 (Figure 22A - Figure 22D) and 622 (Figure 23A - Figure 23D), the IL-2Rγ component is 5', followed by the IL4Rα component and then the Fc component. For the IL-6 traps, 412 (Figure 24A - Figure 24F) and 616 (Figure 25A - Figure 25F), the IL-6Rα component is 5' followed by the gp130 component and then the Fc domain. For the IL-1 trap 569 (Figure 26A - Figure 26E), the IL-1RAcP component is 5' followed by the IL-1RI component and then the Fc domain. The final constructs were cloned into the mammalian expression vector pCDNA3.1 (STRATAGENE).

In the 569 sequence (Figure 26A - Figure 26E), nucleotides 1-1074 encode the IL1RAcP component, nucleotides 1075 -1098 encode a linker region, nucleotides 1099-2043 encode the IL1RI component and nucleotides 2044-2730 encode the Fc domain.

In the 412 sequence (Figure 24A - Figure 24F), nucleotides 1-993 encode the IL6Rα component, nucleotides 994-1023 encode a linker region, nucleotides 1024-2814 encode the gp130 component and nucleotides 2815-3504 encode the Fc domain.

In the 616 sequence (Figure 25A - Figure 25F), nucleotides 1-993 encode the IL6Rα component, nucleotides 994-2784 encode the gp130 component and nucleotides 2785-3474 encode the Fc domain.

In the 424 (Figure 21A - Figure 21D) and 622 (Figure 23A - Figure 23D) sequences, nucleotides 1-762 encode the IL2Rγ component, nucleotides 763-771 encode a linker region, nucleotides 772-1395 encode the IL4Rα component and nucleotides 1396-2082 encode the Fc domain.

Finally, in the 603 sequence (Figure 22A - Figure 22D), nucleotides 1-762 encode the IL2Rγ component, nucleotides 763-1386 encode the IL4Rα component and nucleotides 1387-2073 encode the Fc domain.

DNA constructs were either transiently transfected into COS cells or stably transfected into CHO cells by standard techniques well known to one of skill in the art. Supernatants were collected and purified by Protein A affinity chromatography and size exclusion chromatography by standard techniques. (See for example Harlow and Lane, Antibodies - A Laboratory Manual, Cold Spring Harbor Laboratory, 1988).

EXAMPLE 7: IL-4 BIOASSAY PROTOCOL USING TF-1 (ATCC) CELLS.

Reagents and Equipment Needed

MTT Dye Solution:

MTT(3-[4,5-Dimethylthiazole-2-yl]) (Sigma catalog# M2128)
Working concentration: Dissolve 5 mg of anhydrous MTT in 200 ml PBS without Ca^{+2}, Mg^{+2}.
Sterile filter and store aliquoted at -20°C

Solubilization Solution:

For 1000 ml, combine 100 g SDS, 950 ml dH_20, 50 ml Dimethyl Formamide, and 850 µl concentrated HCl.
Filter sterilize with a 0.45µm filter unit.
Store at room temperature

TF-1 cell Growth Medium:

RPMI 1640, 10% FBS, Pen/Strep, 2mM L-glutamine

Other:

0.4% Trypan Blue Stain, sterile tubes for dilutions, sterile 96 well cell culture plates (Falcon #3072), hemacytometer, centrifuge, ELISA plate reader, multichannel pipet for 15, 25, 50 and 100µl volume, sterile reagent reservoirs, sterile pipet tips, gloves.

Assay Protocol

A. Preparation of Assay plates

1. Prepare sterile 96 well tissue culture plates to contain 50µl of growth medium per well with various concentrations of IL-4 and 10nM IL-4 antagonist. This can be done by preparing a working dilution of IL-4 that is 4 times the highest concentration to be assayed. In separate tubes, do a two-fold serial dilution of the IL-4. Add 25µl of each dilution to one row across the plate (i.e. row A gets highest concentration, row G gets lowest concentration). Add 25µl of growth medium without IL-4 to row H. Prepare the antagonists to be tested by making a stock that is 4 times the final concentration. Add 25µl to a triplicate set of IL-4 containing wells (columns 1,2,3, A through H). Be sure to include antagonist in row H.

2. As a positive control, leave one set with no antagonist. These wells will contain IL-4 and media only.

3. Incubate the plate for 1-2 hours at 37°C in a humidified 5% CO_2 incubator before preparing cells to be used for assay.

B. Preparation of Cells

4. Wash cells twice by centrifugation in assay medium free of growth factor.

5. Determine cell number and trypan blue viability and suspend cells to a final concentration of 8×10^5/ml in assay medium.

6. Dispense 50µl of the cell suspension (40,000 cells) into all wells of the plates. Total volume should now be 100µl/well.

7. Incubate the plate at 37°C for 68 hours in a humidified 5% CO_2 incubator.

C. Color Development

8. After incubating for 68 hours, add 15µl of the MTT dye solution to each well.

9. Incubate the plate at 37°C for 4 hours in a humidified 5% CO_2 incubator.

10. After 4 hours, add 100µl of the solubilization solution to each well. Allow the plate to stand overnight in a sealed container to completely solubilize the formazan crystals.

11. Record the absorbance at 570/650nm.

RESULTS

Figure 27 shows that an IL-4 trap designated 4SC375, which is a fusion polypeptide of IL-2Rγ-scb-IL4Rα-FcΔC1, is several orders of magnitude better as an IL-4 antagonist than IL4RαFcΔC1 alone in the TF1 cell bioassay.

Figure 28 shows that the IL-4 trap designated 4SC375 shows antagonistic activity in the TF1 cell bioassay equivalent to an IL-4 trap designated 4SC424 which is a fusion polypeptide of IL-2Rγ-IL4Rα-FcΔC1 having the IL-2Rγ component flush with the IL-4Rα component.

EXAMPLE 8: IL-6 BIOASSAY PROTOCOL USING XG-1 CELLS

Reagents and Equipment Needed

MTT Dye Solution:

MTT(3-[4,5-Dimethylthiazole-2-yl]) (Sigma catalog# M2128)
Working concentration: Dissolve 5 mg of anhydrous MTT in 200 ml PBS without Ca^{+2}, Mg^{+2}.
Sterile filter and store aliquoted at -20°C

Solubilization Solution:

For 1000 ml, combine 100 g SDS, 950 ml dH_20, 50 ml Dimethyl Formamide, and 850 µl concentrated HCl.
Filter sterilize with at 0.45µm filter unit.
Store at room temperature

Assay Medium:

RPMI 1640, 10%FBS, Pen/Strep, 2mM L-glutamine, 50µM mercapto-ethanol.

Other:

0.4% Trypan Blue Stain, sterile tubes for dilutions, sterile 96 well cell culture plates (Falcon#3072), hemacytometer, centrifuge, ELISA plate reader, multichannel pipet for 15, 25, 50 and 100µl volume, sterile reagent reservoirs, sterile pipet tips, gloves.

Assay Protocol

A. Preparation of Assay plates

1. Prepare sterile 96 well tissue culture plates to contain 50µl of growth medium per well with various concentrations of IL-6 and 10nM IL-6 antagonist. This can be done by preparing a working dilution of IL-6 that is

4 times the highest concentration to be assayed. In separate tubes, do a two-fold serial dilution of the IL-6. Add 25µl of each dilution to one row across the plate (i.e. row A gets highest concentration, row G gets lowest concentration). Add 25µl of growth medium without IL-6 to row H. Prepare the antagonists to be tested by making a stock that is 4 times the final concentration. Add 25µl to a triplicate set of IL-6 containing wells (columns 1,2,3, A through H). Be sure to include antagonist in row H. A typical IL-6 titration starts at 200ng/ml down to 3.1ng/ml.

2. As a positive control, leave one set with no antagonist. These wells contain IL-6 and media in place of antagonist.

3. Incubate the plate 1-2 hours at 37oC in a humidified 5% CO_2 incubator before preparing cells to be used for assay.

B. Preparation of Cells

4. Wash cells twice by centrifugation (5 min at 1000RPM) in assay medium free of growth factor.

5. Determine cell number and trypan blue viability and suspend cells to a final concentration of 8×10^5/ml in assay medium.

6. Dispense 50µl of the cell suspension (40000 cells) into all wells of the plates. Total volume should now be 100µl/well.

7. Incubate the plate at 37°C for 68 hours in a humidified 5% CO_2 incubator.

C. Color Development

8. At 68 hours add 15µl of the dye solution to each well.

9. Incubate the plate at 37°C for 4 hours in a humidified 5% CO_2 incubator.

10. After 4 hours, add 100µl of the solubilization solution to each well. Allow the plate to stand overnight in a sealed container to completely solubilize the formazan crystals.

11. Record the absorbance at 570/650nm.

RESULTS

Figure 29 shows that the IL6 trap (6SC412 IL6R-scb-gpx-FcΔC1) described in Figure 24A - Figure 24F is a better antagonist of IL-6 in the XG1 bioassay than the neutralizing monoclonal antibody to human IL-6 - BE8.

EXAMPLE 9: MRC5 BIOASSAY FOR IL1 TRAPS

MRC5 human lung fibroblast cells respond to IL-1 by secreting IL-6 and thus were utilized to assay the ability of IL-1 traps to block the IL-1-dependent production of IL-6. IL1 Trap 1SC569 (Figure 26A - Figure 26E) was tested against IL-1-RI.Fc which is the extracellular domain of the IL-1 Type I receptor fused to an Fc domain.

MRC5 cells are suspended at 1×10^5 cells per ml in medium and 0.1 ml of cells are plated (10,000 cells per well) into the wells of a 96 well tissue culture plate. Plates are incubated for 24 hours at 37°C in a humidified 5% CO_2 incubator.

IL-1 trap and recombinant human IL-1 at varying doses are pre-incubated in a 96 well tissue culture dish and incubated for 2 hours at 37°C. 0.1 ml of this mixture is then added to the 96 well plate containing the MRC5 cells such that the final concentration of IL-1 Trap is 10nM and the final

concentrations of the IL-1 ranges from 2.4 pM to 5nM. Control wells contain trap alone or nothing.

Plates are then incubated at 37°C for 24 hours in a humidified 5% CO_2 incubator. Supernatant is collected and assayed for levels of IL-6 using R&D Systems Quantikine Immunoassay Kit according to the manufacturer's instructions.

RESULTS

Figure 30 shows that the trap 569 (Figure 26A - Figure 26E) is able to antagonize the effects of IL-1 and block the IL-6 production from MRC 5 cells upon treatment with IL-1. At a concentration of 10nM, the trap 569 is able to block the production of IL-6 up to an IL-1 concentration of 3nM. In contrast, the IL-1RI.Fc is a much poorer antagonist of IL-1. It is only able to block the effects of IL-1 up to about 10-20 pM. Thus, the trap 569 is approximately 100x better at blocking IL-1 than IL1RI.Fc.

EXAMPLE 10 - CONSTRUCTION OF IL-13/IL-4 SINGLE CHAIN TRAPS

1. To create the IL-13/IL-4 dual trap designated IL-4Rα.IL-13Rα1.Fc, the human IL-4Rα extracellular domain (corresponding to nucleotides #1-693 of Figure 31A - Figure 31G) and the human IL-13Rα1 extracellular domain (corresponding to nucleotides #700-1665 of Figure 31A - Figure 31G) were amplified by standard PCR techniques and ligated into an expression vector pMT21 which contained the human Fc sequence (corresponding to nucleotides #1671-2355 of Figure 31A - Figure 31G), thus creating a fusion protein consisting of the IL-4Rα , IL-13Rα1, and the hinge, CH2 and CH3 region of human IgG1 from the N to C terminus. In addition, a two amino acid linker (corresponding to nucleotides #694-699 of Figure 31A - Figure 31G) with the amino acid sequence SerGly was constructed in frame

between the IL-4Rα and the IL-13Rα1 and a two amino acid linker (corresponding to nucleotides #1666-1671 of Figure 31A - Figure 31G) with the amino acid sequence ThrGly was constructed in frame between the IL-13Rα1 and the Fc portion. All sequences were sequence-verified by standard techniques. The IL-4Rα.IL-13Rα1.Fc coding sequence was then subcloned into the expression vector pCDNA3.1 (Stratagene) using standard molecular biology techniques.

2. To create the IL-13/IL-4 dual trap designated IL-13Rα1.IL-4Rα.Fc, the IL-13Rα1 extracellular domain (corresponding to nucleotides #1-1029 of Figure 32A - Figure 32G) and the human IL-4Rα (corresponding to nucleotides # 1060-1692 of Figure 32A - Figure 32G) were amplified by standard PCR techniques and ligated into the expression vector pJFE14, which contains the human Fc sequence (corresponding to nucleotides #1699-2382 of Figure 32A - Figure 32G) to create a fusion protein consisting of the IL-13Rα1, IL-4Rα, and the hinge, CH2 and CH3 region of human IgG1 from the N to C terminus. In addition, a ten amino acid linker with the amino acid sequence GlyAlaProSerGlyGlyGlyGlyArgPro (corresponding to nucleotide #1030-1059 of Figure 32A - Figure 32G) was constructed in frame between the IL-13Rα1 and the IL-4Rα and a two amino acid linker (corresponding to nucleotides #1693-1698 of Figure 32A - Figure 32G) with the amino acid sequence SerGly was constructed in frame between IL-4Rα and the Fc portion. All sequences were sequence-verified using standard techniques. The coding sequence of IL-13Rα1.IL-4Rα.Fc was then subcloned into the expression vector pCDNA3.1 (Stratagene) using standard molecular biology techniques.

EXAMPLE 11: EXPRESSION OF IL-4Rα.IL-13Rα1.Fc AND IL-13Rα1.IL-4Rα.Fc

Large scale (1L) cultures of the pCAE801 (the DNA vector construct encoding IL-4Rα.IL-13Rα1.Fc) and pCAE802 (the DNA plasmid construct encoding IL-13Rα1.IL-4Rα.Fc) in DH10B cells were grown overnight in LB + ampicillin and the plasmid DNA was extracted using a Qiagen Endofree Mega Kit following the manufacturer's protocol. The concentration of the purified plasmid DNA was determined in a UV spectrophotometer and fluorometer. The plasmid DNA was also verified by digestion of aliquots with BbsI, XmnI and NcoI restriction enzymes. All restriction enzyme digest fragments corresponded to the predicted sizes in a 1% agarose gel.

Forty 15 cm petri plates were seeded with CHO-K1/E1A cells at a density of 4×10^6 cells/plate. Plating media was Gibco Ham's F-12 w/10% Hyclone Fetal Bovine Serum (FBS) + penicillin/streptomycin and supplemented with glutamine. The following day each plate was transfected with 6 μg of pCAE801, or pCAE802, using Gibco Optimem and Gibco Lipofectamine in 12 ml volume, following the manufacturer's protocol. Four hours after adding the transfection mix to the cells 12 ml/plate of Optimem w/ 10% FBS was added. Plates were incubated at 37°C in a 5% CO_2 incubator overnight. The following day the media was removed from each plate and 25 ml expression media (Gibco CHO-S-SFM II w/ glutamine + 1mM sodium butyrate) was added. The plates were incubated at 37°C for 3 days.

After 3 days of incubation the media was removed from each plate and centrifuged at 400 rpm in a swinging bucket rotor to pellet cells. The supernatant was decanted into sterile 1L bottles and expressed protein was purified as described *infra*.

EXAMPLE 12: PURIFICATION OF IL-4Rα.IL-13Rα1.Fc AND IL-13Rα1.IL-4Rα.Fc PROTEIN FROM CULTURE MEDIA

1. Purification of IL-4Rα.IL-13Rα1.Fc.

Human IL-4Rα.IL-13Rα1.Fc was transiently expressed in CHO cells and supernatants were harvested from plate transfections as described *supra*. Expression of the secreted protein was determined by a sandwich ELISA using goat anti-hIgG (γ chain specific; Sigma 1-3382) and goat anti-hIgG (Fc specific)-FITC conjugate (Sigma F9512) capture and report antibodies, respectively. The yield ranged from 5.8 to 9.2 mg (average of 7.5 mg) per liter of conditioned media. Complete™ protease inhibitor tablets (Roche Diagnostics Corp.) were dissolved into the media (1 tablet/L). The conditioned media was sterile filtered (0.22 μm pore size) prior to loading onto a pre-equilibrated, 5 mL HiTrap® Protein A affinity column (Amersham Pharmacia Biotech) in Dulbecco's PBS buffer (Life Technologies), pH 7.4 at 4°C. The flow rate was ~1-2 mL/min. The column was extensively washed with PBS buffer to remove nonspecifically bound proteins from the column. IL-4Rα.IL-13Rα1.Fc was eluted using 20 mM sodium citrate, 150 mM NaCl, pH 3.5. The eluate was immediately neutralized by titrating with 1 M Tris-OH. The fractions containing protein were pooled and immediately dialyzed in PBS buffer, pH 7.4 at 4°C. The recovery from Protein A purification was 6.8 mg (73%). IL-4Rα.IL-13Rα1.Fc was further purified by size exclusion chromatography using a superose 6 column (25 mL bed volume; Amersham Pharmacia Biotech) pre-equilibrated in PBS, 5% v/v glycerol, pH 7.4 at ambient temperature. The flow rate was 0.5 mL/min. Protein fractions were assessed from a Coomassie stained non-reduced and reduced SDS-PAGE (Novex NuPAGE 4-12% Bis-Tris gels). Fractions were conservatively pooled to reduce the amount of aggregated protein. The overall yield was 51% (4.4 mg) with a purity of 97% as judged by SDS-PAGE. Purified IL-4Rα.IL-13Rα1.Fc was analyzed by non-reduced and reduced SDS-PAGE (4-12% Bis-Tris), analytical size exclusion chromatography (Tosohaas

TSKG4000SWXL), N-terminal sequencing, and immunoblotting with goat anti-hIgG-HRP conjugate (Promega W403B), and also mouse monoclonal anti-hIL-4R (R&D MAB230) followed by anti-mIgG-HRP conjugate (Promega W402B) as the secondary antibody.

2. Purification of IL-13Rα1.IL-4Rα.Fc

Human IL-13Rα1.IL-4Rα.Fc was transiently expressed in CHO cells and supernatants were harvested from plate transfections as described *supra*. Expression of the secreted protein was determined by a sandwich ELISA using goat anti-hIgG (γ chain specific; Sigma 1-3382) and goat anti-hIgG (Fc specific)-FITC conjugate (Sigma F9512) capture and report antibodies, respectively. The yield was 8.8 mg per liter of conditioned media. Complete™ protease inhibitor tablets (Roche Diagnostics Corp.) were dissolved into the media (1 tablet/L). The conditioned media was sterile filtered (0.22 μm pore size) prior to loading onto a pre-equilibrated, 5 mL HiTrap® Protein A affinity column (Amersham Pharmacia Biotech) in Dulbecco's PBS buffer (Life Technologies), pH 7.4 at 4°C. The flow rate was ~1-2 mL/min. The column was extensively washed with PBS buffer to remove nonspecifically bound proteins from the column. IL-13Rα1.IL-4Rα.Fc was eluted using 20 mM sodium citrate, 150 mM NaCl, pH 3.5. The eluate was immediately neutralized by titrating with 1 M Tris-OH. The fractions containing protein were pooled and immediately dialyzed in PBS buffer, pH 7.4 at 4 °C. The recovery from Protein A purification was 3.8 mg (43%). IL-13Rα1.IL-4Rα.Fc was further purified by size exclusion chromatography using a superose 6 column (25 mL bed volume; Amersham Pharmacia Biotech) pre-equilibrated in PBS, 5% v/v glycerol, pH 7.4 at ambient temperature. The flow rate was 0.5 mL/min. Protein fractions were assessed from a Coomassie stained non-reduced and reduced SDS-PAGE (Novex NuPAGE 4-12% Bis-Tris gels). Fractions were

conservatively pooled to reduce the amount of aggregated protein. The overall yield was 17% (1.5 mg) with a purity of 95% as judged by SDS-PAGE. Purified IL-13Rα1.IL-4Rα.Fc was analyzed by non-reduced and reduced SDS-PAGE (4-12% Bis-Tris), analytical size exclusion chromatography (Tosohaas TSKG4000SWXL), N-terminal sequencing, and immunoblotting with goat anti-hIgG-HRP conjugate (Promega W403B), and also mouse monoclonal anti-hIL-4Rα (R&D MAB230) followed by anti-mIgG-HRP conjugate (Promega W402B) as the secondary antibody.

EXAMPLE 13: BLOCKING OF IL-4 AND IL-13 BY IL-4Rα.IL-13Rα1.Fc AND IL-13Rα1.IL-4Rα.Fc

Materials and Methods

TF1 Bioassay. TF1 cells were maintained in growth media (10ng/ml GM-CSF, RPMI 1640, 10% FBS, L-glutamine, Penicillin, Streptomycin). For the bioassay, cells were washed 2 times in assay media (as above but without GM-CSF) and then plated at 2 x 10^5 cells in 50µl of assay media. The purified IL-4Rα.IL-13Rα1.Fc and IL-13Rα1.IL-4Rα.Fc proteins were diluted into assay media at a concentration of 40nM. 25ul of each of the traps was added to the cells. Either IL-13 or IL-4 were diluted to 40nM in assay media and then 2-fold dilution series in assay media were made. 25µl of either IL-13 or IL-4 was then added to the wells containing the cells and the traps. Cells were then incubated at 37°C, 5% CO_2 for ~70 hrs. The extent of TF1 cell proliferation was measured by the MTS assay according to the manufacturer's protocol (Promega, Inc.).

RESULTS

The ability of the IL-4Rα.IL-13Rα1.Fc and IL-13Rα1.IL-4Rα.Fc traps to block both human IL-13 and human IL-4 activity was measured in the TF1

bioassay described *supra*. IL-13 stimulates proliferation of TF1 cells, with half-maximal growth at a concentration of 0.2nM. Addition of either IL-4Rα.IL-13Rα1.Fc or IL-13Rα1.IL-4Rα.Fc trap at a concentration of 10nM blocks IL-13-induced growth up to ~2nM (Figure 33). At an IL-13 concentration of ~4-5 nM the growth of TF1 cells is inhibited by 50%. TF1 cells are more sensitive to IL-4, which stimulates their proliferation with half-maximal growth at ~0.02nM. Addition of either IL-4Rα.IL-13Rα1.Fc or IL-13Rα1.IL-4Rα.Fc at a concentration of 10nM blocks IL-4-induced growth up to ~1nM (Figure 34). At an IL-4 concentration of ~3-4 nM the growth of TF1 cells is inhibited by 50%. These results show that both IL-4Rα.IL-13Rα1.Fc and IL-13Rα1.IL-4Rα.Fc can block the ability of both IL-13 and IL-4 to stimulate cellular responses.

EXAMPLE 14: BLOCKING OF INJECTED IL-1 BY IL-1 TRAP *IN VIVO*

IL-1 is a pro-inflammatory cytokine. Systemic administration of IL-1 has been shown to elicit acute responses in animals, including transient hyperglycemia, hypoinsulinemia, fever, anorexia, and increased serum levels of interleukin-6 (IL-6) (Reimers, 1998). Since mice are responsive to both murine and human IL-1, human IL-1 can be used and *in vivo* binding effects of human specific IL-1 antagonists can be evaluated. This acute mouse model was used to determine the ability of a human IL-1 trap to antagonize the *in vivo* effects of exogenously administered human IL-1. This provides a rapid indication of *in vivo* efficacy of the human IL-1 trap and can be used as an assay to help molecule selection.

Experimental Design:

Mice were given subcutaneous injections of human IL-1 (0.3 μg/kg). Twenty-four hours prior to human IL-1 injection, the animals were pre-treated with either vehicle or 150-fold molar excess of human IL-1 trap (0.54 mg/kg). Two hours prior to sacrifice (26 hrs), the mice were given a

second injection of human IL-1 (0.3 μg/kg). Blood samples were collected at various time points and sera were assayed for IL-6 levels.

RESULTS

Exogenous administration of human IL-1 resulted a dramatic induction of serum IL-6 levels. At 150-fold molar excess, the human IL-1 trap completely blocked the IL-6 increase (Figure 35). Furthermore, the effects of the human IL-1 trap persisted for at least another 24 hours, preventing an IL-6 increase even when IL-1 was re-administered (Figure 35). Such long-lasting efficacy suggests that daily injection of an IL-1 trap may not be necessary for chronic applications.

EXAMPLE 15: EVALUATING THE ABILITY OF AN IL-4 TRAP TO BLOCK THE PHYSIOLOGICAL RESPONSES TO HUMAN IL-4 IN CYNOMOLOGUS MONKEYS.

Systemic administration of human IL-4 elicits systemic responses in Cynomologus monkeys (Gundel et al., 1996). Thus, the effectiveness of the IL-4 trap in blocking human IL-4 can be demonstrated by measuring these responses.

Experimental Design:

The experiment consisted of 3 parts: human IL-4 + vehicle (part 1), human IL-4 + IL-4 Trap (part 2), and human IL-4 + vehicle (part 3). Human IL-4 (25 μg/kg) was injected subcutaneously twice daily for 4 days and IL-4 Trap (8 mg/kg) and vehicle were given intravenously daily for 5 days, beginning 1 day prior to human IL-4 administration. Whole blood was collected daily for flow cytometry analysis for CD16 and plasma was obtained to assay for the cytokine monocyte chemotactic protein 1 (MCP-1).

CD16 and MCP-1 are markers of IL-4-mediated inflammation in both humans and monkeys.

RESULTS

In the presence of human IL-4, MCP-1 increased 2.5-fold and was significantly blocked by the IL-4 Trap (Figure 36A). Similarly, the decrease in the percent of CD16 positive lymphocytes in peripheral blood was attenuated by the IL-4 trap (Figure 36B). After a rest period, the monkeys were re-injected with human IL-4 and the responsiveness of the animals to human IL-4 was re-confirmed (Figures 36A and 36B), suggesting that inhibition of the MCP-1 and CD 16 responses is specifically mediated by the IL-4 trap.

EXAMPLE 16: THE EFFECTS OF IL-4 TRAP ON 1L-4-INDUCED IgE SECRETION.

It has been shown that injection of anti-mouse IgD antibody stimulates an IL-4-mediated IgE increase in normal mice. This model has been widely used to evaluate IL-4 antagonists, such as soluble IL-4 receptor and anti-IL-4 monoclonal antibodies (Sato et al., 1993). We decided to use this model to evaluate the ability if the IL-4 trap to block IL-4-mediated increases of IgE.

Experimental design:

BALB/C mice injected with anti-mouse IgD (100µl/mouse, s.c.) were randomly divided into 3 groups. Each received (on days 3-5) either vehicle, murine IL-4 trap (1 mg/kg, s.c.), or a monoclonal antibody to mouse IL-4 (1 mg/kg, s.c.). Serum was collected at various time points and assayed for IgE levels.

RESULTS

Treatment with the murine IL-4 trap or the mouse IL-4 antibody both significantly antagonized the IL-4-mediated IgE increase in this mouse model (Figure 37). This suggests that the murine IL-4 trap binds murine IL-4 and antagonizes physiological responses elicited by endogenous IL-4 *in vivo*.

The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

WE CLAIM:

1. An isolated nucleic acid molecule encoding a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex comprising:

a) a nucleotide sequence encoding a first fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the specificity determining component of the cytokine's receptor;

b) a nucleotide sequence encoding a second fusion polypeptide component comprising the amino acid sequence of the cytokine binding portion of the extracellular domain of the signal transducing component of the cytokine's receptor; and

c) a nucleotide sequence encoding a third fusion polypeptide component comprising the amino acid sequence of a multimerizing component.

2. The nucleic acid molecule of claim 1, wherein the nucleotide sequence encoding the first component is upstream of the nucleotide sequence encoding the second component.

3. The nucleic acid molecule of claim 1, wherein the nucleotide sequence encoding the first component is downstream of the nucleotide sequence encoding the second component.

4. The isolated nucleic acid molecule of claim 1, wherein the cytokine receptor is the receptor for a member of the hematopoietin family of cytokines selected from the group consisting of interleukin-2, interleukin-3, interleukin-4, interleukin-5, interleukin-6, interleukin-7, interleukin-9, interleukin-11, interleukin-13, interleukin-15, granulocyte macrophage colony stimulating factor, oncostatin M, and leukemia inhibitory factor and cardiotrophin-1

5. The isolated nucleic acid molecule of claim 1, wherein the cytokine receptor is the receptor for a member of the interferon family of cytokines selected from the group consisting of IFN-gamma, IFN-alpha, and IFN-beta.

6. The isolated nucleic acid molecule of claim 1, wherein the cytokine receptor is the receptor for a member of the immunoglobulin superfamily of cytokines selected from the group consisting of B7.1 (CD80) and B7.2 (B70).

7. The isolated nucleic acid molecule of claim 1, wherein the cytokine receptor is the receptor for a member of the TNF family of cytokines selected from the group consisting of TNF-alpha, TNF-beta, LT-beta, CD40 ligand, Fas ligand, CD 27 ligand, CD 30 ligand, and 4-1BBL.

8. The isolated nucleic acid molecule of claim 1, wherein the cytokine receptor is the receptor for a member of the TGF-β/BMP family selected from the group consisting of TGF-β1, TGF-β2, TGF-β3, BMP-2, BMP-3a, BMP-3b, BMP-4, BMP-5, BMP-6, BMP-7, BMP-8a, BMP-8b, BMP-9, BMP-10, BMP-11, BMP-15, BMP-16, endometrial bleeding associated factor (EBAF), growth differentiation factor-1 (GDF-1), GDF-2, GDF-3, GDF-5, GDF-6, GDF-7, GDF-8, GDF-9, GDF-12, GDF-14, mullerian inhibiting substance (MIS), activin-1, activin-2, activin-3, activin-4, and activin-5.

9. The isolated nucleic acid molecule of claim 1, wherein the cytokine receptor is the receptor for a cytokine selected from the group consisting of interleukin-1, interleukin-10, interleukin-12, interleukin-14, interleukin-18 and MIF.

10. The isolated nucleic acid molecule of claim 1, wherein the multimerizing component comprises an immunoglobulin derived domain.

11. The isolated nucleic acid molecule of claim 10, wherein the immunoglobulin derived domain is selected from the group consisting of the Fc domain of IgG, the heavy chain of IgG, and the light chain of IgG.

12. A fusion polypeptide encoded by the isolated nucleic acid molecule of claim 1.

13. A composition capable of binding a cytokine to form a nonfunctional complex comprising a multimer of the fusion polypeptide of claim 12.

14. The composition of claim 13, wherein the multimer is a dimer.

15. A vector which comprises the nucleic acid molecule of claim 1.

16. An expression vector comprising a nucleic acid molecule of claim 1, wherein the nucleic acid molecule is operatively linked to an expression control sequence.

17. A host-vector system for the production of a fusion polypeptide which comprises the expression vector of claim 16, in a suitable host cell.

18. The host-vector system of claim 17, wherein the suitable host cell is a bacterial cell, yeast cell, insect cell, or mammalian cell.

19. The host-vector system of claim 17, wherein the suitable host cell is E. coli.

20. The host-vector system of claim 17, wherein the suitable host cell is a COS cell.

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21. The host-vector system of claim 17, wherein the suitable host cell is a CHO cell.

22. The host-vector system of claim 17, wherein the suitable host cell is a 293 cell.

23. The host-vector system of claim 17, wherein the suitable host cell is a BHK cell.

24. The host-vector system of claim 17, wherein the suitable host cell is a NS0 cell.

25. A method of producing a fusion polypeptide which comprises growing cells of the host-vector system of claim 17, under conditions permitting production of the fusion polypeptide and recovering the fusion polypeptide so produced.

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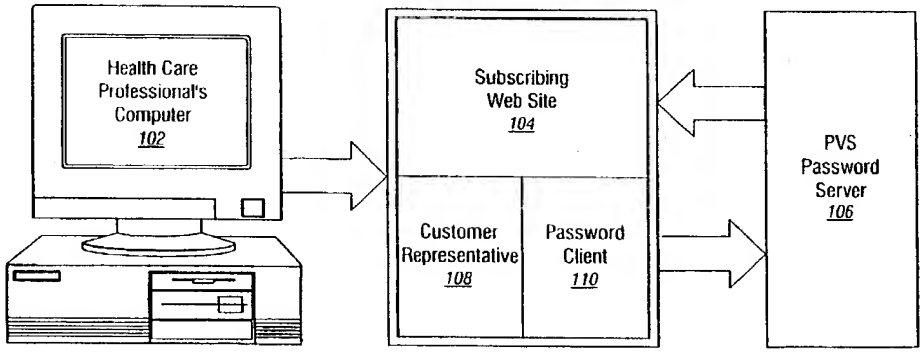
(54) Title: REMOTE PHYSICIAN AUTHENTICATION SERVICE



(57) Abstract

A method and system of remote verification of an end user of web page with controlled access. Users are issued a user name and password which can be used to access any site which subscribes to the described verification system. A user connects to a web site which contains desired information. When the user attempts to enter an area (or page) of the site with controlled access the pre–issued user name and password are requested. Once this information is entered, the subscribing website sends a secure (encrypted) query to a remote password database server. The supplied information is checked against a verification database. A yes or no secure verification is sent back to the subscriber site. This verification can include anonymized demographic information such as specialty, location, and type of practice. The subscriber site then acts upon the verification received. The information entred by the user, while sent by the subscribing site is not accessible by the subscribing site. Thus, the subscribing site cannot create its own database of pre–verified users. Preferably users are not required to be preregistered, and can gain access by entering identifiers which are checked against official Medical Association records. Preferably, whenever a user accesses a Web site and provides basic demographic data, the image of the sales representative most likely to deal with that user (based on location, zip code, or area of interest, etc.) will appear on the user's screen. The web site gets enough of the data entered by the user to select the proper sales representative, but not enough to target the user with solicitations.

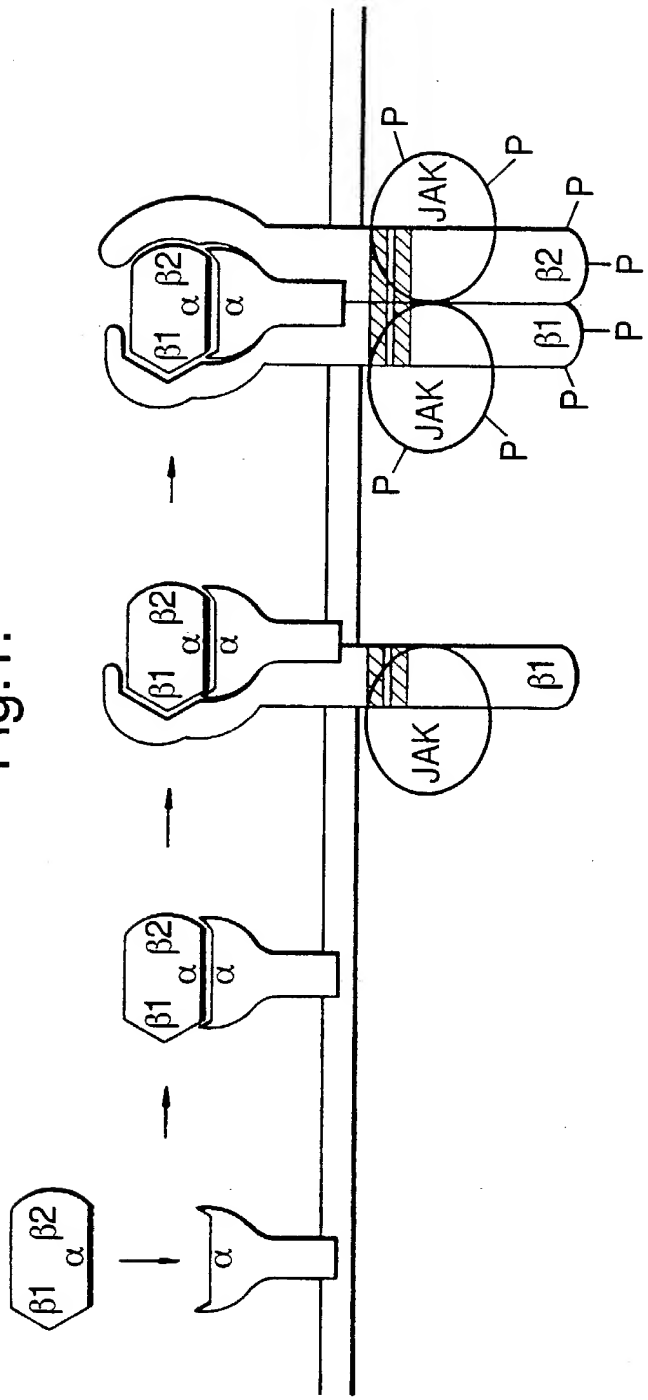


Fig.1.

Fig.2.

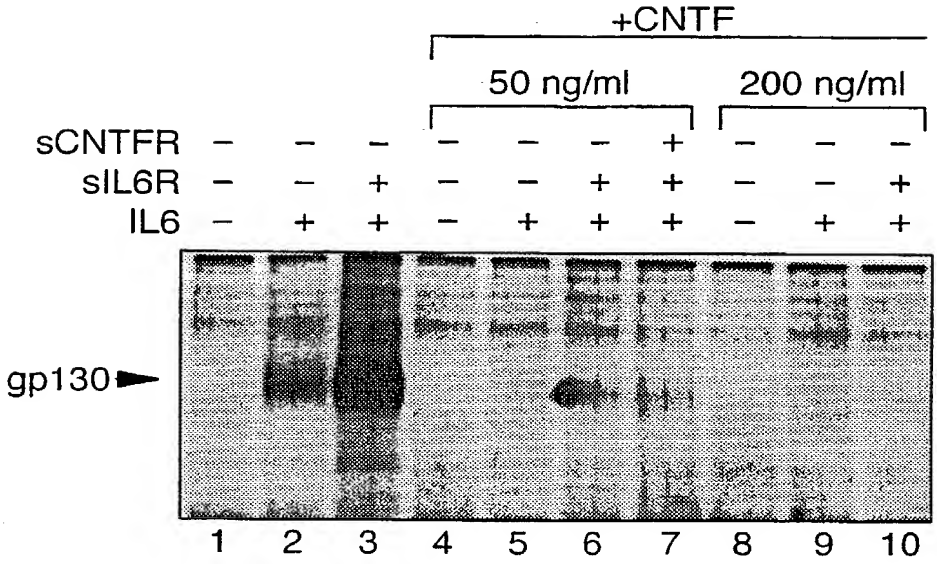

+CNTF
50 ng/ml
200 ng/ml
sCNTFR – – – – – – + – – –
sIL6R – – + – – + + – – +
IL6 – + + – + + + – + +
gp130
1 2 3 4 5 6 7 8 9 10

Fig.3.

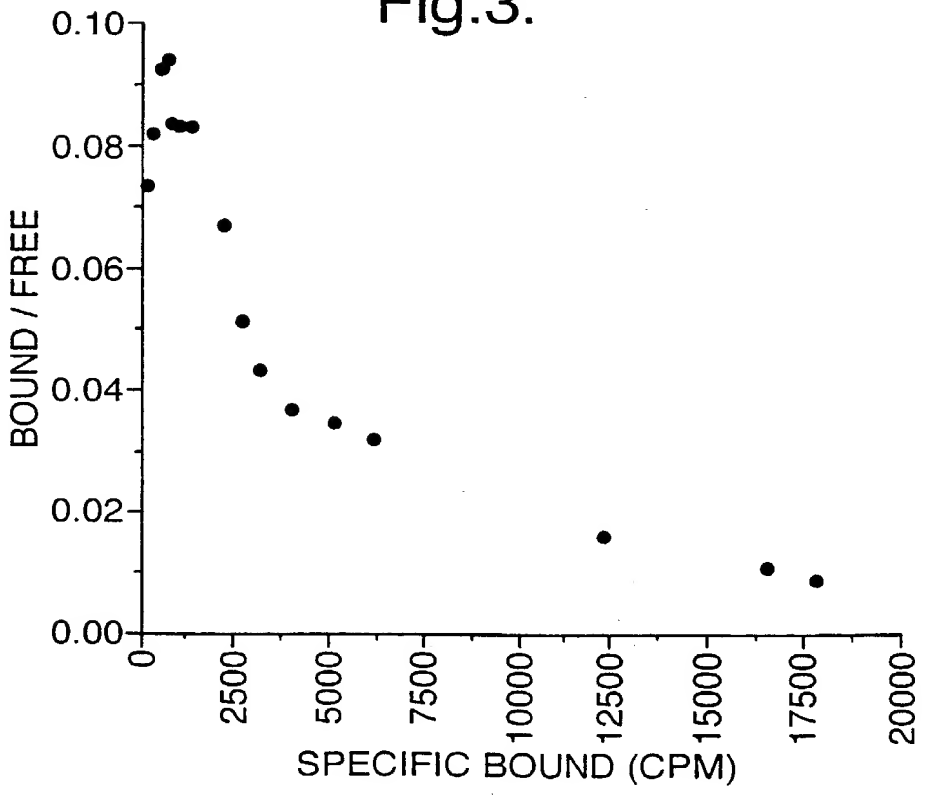

BOUND / FREE
0.10
0.08
0.06
0.04
0.02
0.00
0
2500
5000
7500
10000
12500
15000
17500
20000
SPECIFIC BOUND (CPM)

Fig.4.

Amino acid sequence of human gp130-Fc-His6

Sequence Range: 1 to 861

```
        10         20         30         40         50         60
         *          *          *          *          *          *
MVTLQTWVVQALFIFLTTES TGELLDPCGYISPESPVVQL HSNFTAVCVLKEKCMDYFHV

        70         80         90        100        110        120
         *          *          *          *          *          *
NANYIVWKTNHFTIPKEQYT IINRTASSVTFTDIASLNIQ LTCNILTFGQLEQNVYGITI

       130        140        150        160        170        180
         *          *          *          *          *          *
ISGLPPEKPKNLSCIVNEGK KMRCEWDGGRETHLETNFTL KSEWATHKFADCKAKRDTPT

       190        200        210        220        230        240
         *          *          *          *          *          *
SCTVDYSTVYFVNIEVWVEA ENALGKVTSDHINFDPVYKV KPNPPHNLSVINSEELSSIL

       250        260        270        280        290        300
         *          *          *          *          *          *
KLTWTNPSIKSVIILKYNIQ YRTKDASTWSQIPPEDTAST RSSFTVQDLKPFTEYVFRIR

       310        320        330        340        350        360
         *          *          *          *          *          *
CMKEDGKGYWSDWSEEASGI TYEDRPSKAPSFWYKIDPSH TQGYRTVQLVWKTLPPFEAN

       370        380        390        400        410        420
         *          *          *          *          *          *
GKILDYEVTLTRWKSHLQNY TVNATKLTVNLTNDRYLATL TVRNLVGKSDAAVLTIPACD

       430        440        450        460        470        480
         *          *          *          *          *          *
FQATHPVMDLKAFPKDNMLW VEWTTPRESVKKYILEWCVL SDKAPCITDWQQEDGTVHRT

       490        500        510        520        530        540
         *          *          *          *          *          *
YLRGNLAESKCYLITVTPVY ADGPGSPESIKAYLKQAPPS KGPTVRTKKVGKNEAVLEWD

       550        560        570        580        590        600
         *          *          *          *          *          *
QLPVDVQNGFIRNYTIFYRT IIGNETAVNVDSSHTEYTLS SLTSDTLYMVRMAAYTDEGG

       610        620        630        640        650        660
         *          *          * t  t     *          *          *
KDGPEFTFTTPKFAQGEIES GEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMIS

       670        680        690        700        710        720
         *          *          *          *          *          *
RTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWL

       730        740        750        760        770        780
         *          *          *          *          *          *
```

Fig.4 (Cont).

NGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPS RDELTKNQVSLTCLVKGFYP

790 800 810 820 830 840

SDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHN

850 860

HYTQKSLSLSPGK*HHHHHH*•

Fig.5.

The amino acid sequence of human IL-6Rα-Fc

Sequence Range: 1 to 594

10 20 30 40 50 60

MVAVGCALLAALLAAPGAAL APRRCPAQEVARGVLTSLPG DSVTLTCPGVEPEDNATVHW

70 80 90 100 110 120

VLRKPAAGSHPSRWAGMGRR LLLRSVQLHDSGNYSCYRAG RPAGTVHLLVDVPPEEPQLS

130 140 150 160 170 180

CFRKSPLSNVVCEWGPRSTP SLTTKAVLLVRKFQNSPAED FQEPCQYSQESQKFSCQLAV

190 200 210 220 230 240

PEGDSSFYIVSMCVASSVGS KFSKTQTFQGCGILQPDPPA NITVTAVARNPRWLSVTWQD

250 260 270 280 290 300

PHSWNSSFYRLRFELRYRAE RSKTFTTWMVKDLQHHCVIH DAWSGLRHVVQLRAQEEFGQ

310 320 330 340 350 360

GEWSEWSPEAMGTPWTESRS PPAENEVSTPMQALTTNKDD DNILFRDSANATSLPVQDAG

370 380 390 400 410 420

EPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKF

430 440 450 460 470 480

NWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKT

490 500 510 520 530 540

ISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTP

550 560 570 580 590

PVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK•

Fig.6.

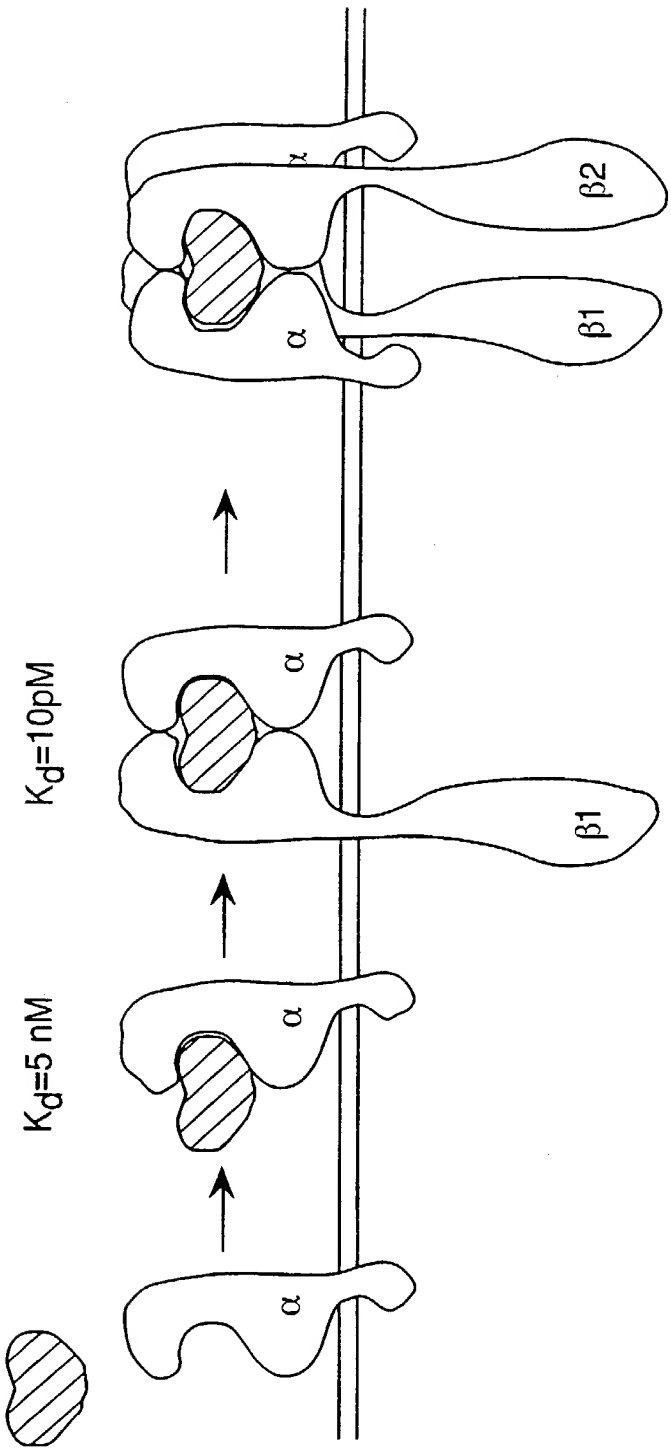
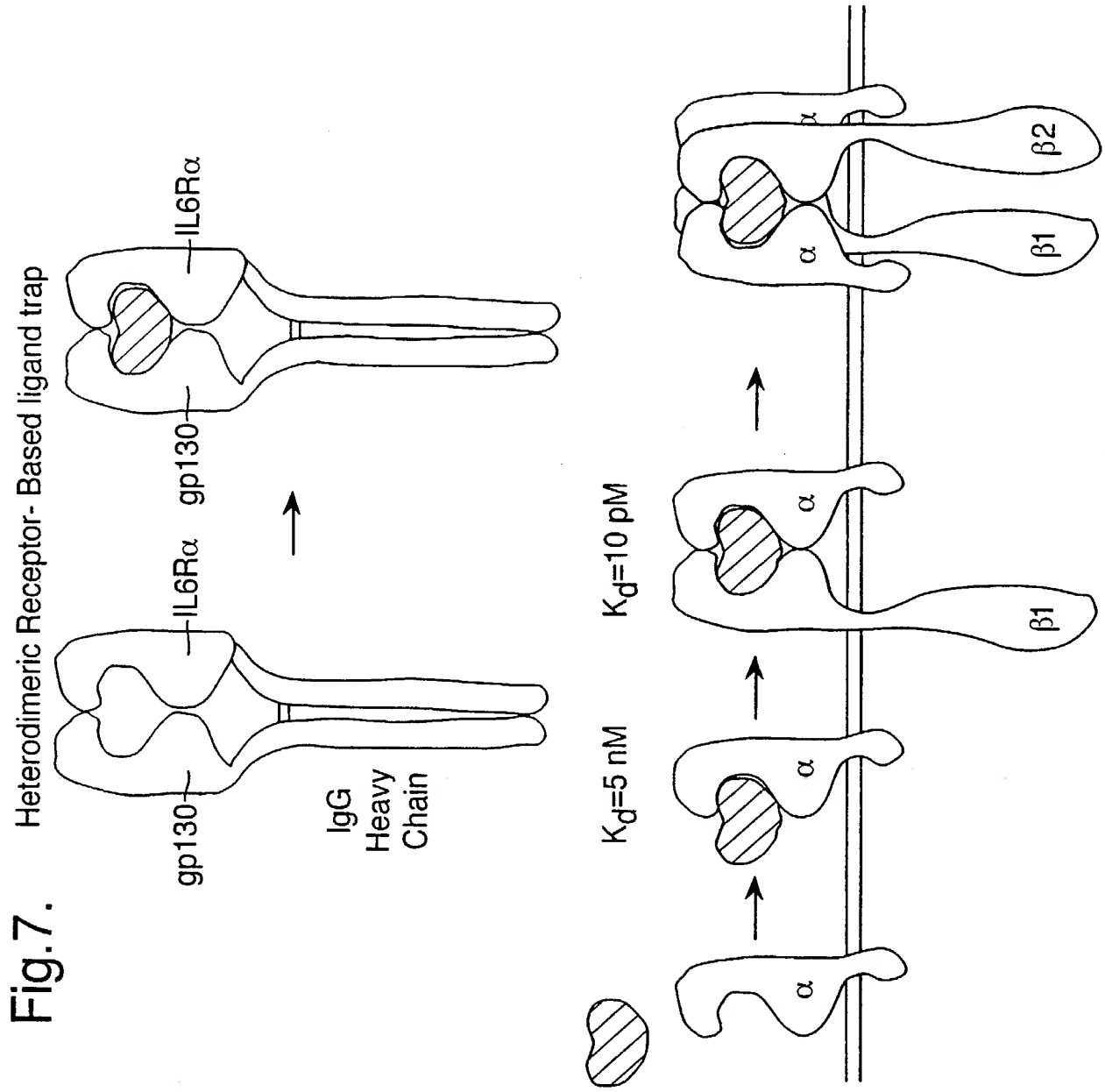


Fig.7.


Heterodimeric Receptor- Based ligand trap
IL6Rα
gp130
IL6Rα
gp130
IgG
Heavy
Chain
K_d=5 nM
K_d=10 pM
α
α
α
α
β1
β1
β2

09767835.032201
09/703835

Fig.8.

Immunoglobulin Heavy/Light Chain receptor Fusions

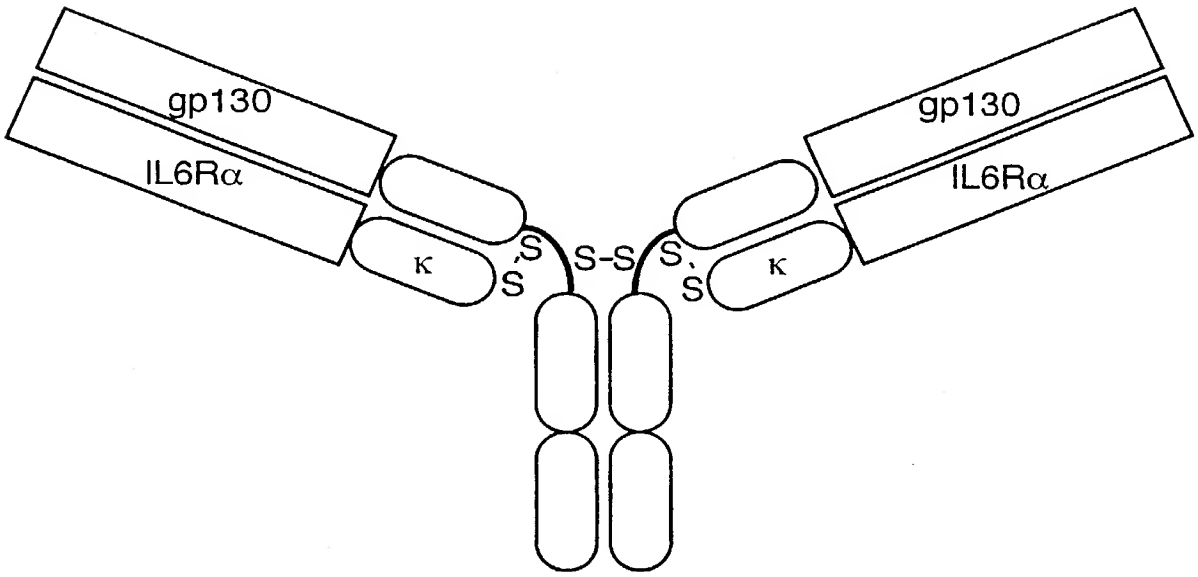


Fig.9.

Amino acid sequence of gp130-Cγ1

Sequence Range: 1 to 952

```
          10         20         30         40         50         60
           *          *          *          *          *          *
MVTLQTWVVQALFIFLTTES TGELLDPCGYISPESPVVQL HSNFTAVCVLKEKCMDYFHV

          70         80         90        100        110        120
           *          *          *          *          *          *
NANYIVWKTNHFTIPKEQYT IINRTASSVTFTDIASLNIQ LTCNILTFGQLEQNVYGITI

         130        140        150        160        170        180
           *          *          *          *          *          *
ISGLPPEKPKNLSCIVNEGK KMRCEWDGGRETHLETNFTL KSEWATHKFADCKAKRDTPT

         190        200        210        220        230        240
           *          *          *          *          *          *
SCTVDYSTVYFVNIEVWVEA ENALGKVTSDHINFDPVYKV KPNPPHNLSVINSEELSSIL

         250        260        270        280        290        300
           *          *          *          *          *          *
KLTWTNPSIKSVIILKYNIQ YRTKDASTWSQIPPEDTAST RSSFTVQDLKPFTEYVFRIR

         310        320        330        340        350        360
           *          *          *          *          *          *
CMKEDGKGYWSDWSEEASGI TYEDRPSKAPSFWYKIDPSH TQGYRTVQLVWKTLPPFEAN

         370        380        390        400        410        420
           *          *          *          *          *          *
GKILDYEVTLTRWKSHLQNY TVNATKLTVNLTNDRYLATL TVRNLVGKSDAAVLTIPACD

         430        440        450        460        470        480
           *          *          *          *          *          *
FQATHPVMDLKAFPKDNMLW VEWTTPRESVKKYILEWCVL SDKAPCITDWQQEDGTVHRT

         490        500        510        520        530        540
           *          *          *          *          *          *
YLRGNLAESKCYLITVTPVY ADGPGSPESIKAYLKQAPPS KGPTVRTKKVGKNEAVLEWD

         550        560        570        580        590        600
           *          *          *          *          *          *
QLPVDVQNGFIRNYTIFYRT IIGNETAVNVDSSHTEYTLS SLTSDTLYMVRMAAYTDEGG

         610        620        630        640        650        660
           *          *          *          *          *          *
KDGPEFTFTTPKFAQGEIES GASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTV

         670        680        690        700        710        720
           *          *          *          *          *          *
SWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVE

         730        740        750        760        770        780
           *          *          *          *          *          *
PKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFN
```

Fig.9 (Cont).

```
       790        800        810        820        830        840
        *          *          *          *          *          *
WYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTI

       850        860        870        880        890        900
        *          *          *          *          *          *
SKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPP

       910        920        930        940        950
        *          *          *          *          *
VLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHY TQKSLSLSPGK*
```

Fig.10.

Amino acid sequence of gp130Δ3fibro

Sequence Range: 1 to 332

```
        10         20         30         40         50         60
         *          *          *          *          *          *
MVTLQTWVVQALFIFLTTES TGELLDPCGYISPESPVVQL HSNFTAVCVLKEKCMDYFHV

        70         80         90        100        110        120
         *          *          *          *          *          *
NANYIVWKTNHFTIPKEQYT IINRTASSVTFTDIASLNIQ LTCNILTFGQLEQNVYGITI

       130        140        150        160        170        180
         *          *          *          *          *          *
ISGLPPEKPKNLSCIVNEGK KMRCEWDGGRETHLETNFTL KSEWATHKFADCKAKRDTPT

       190        200        210        220        230        240
         *          *          *          *          *          *
SCTVDYSTVYFVNIEVWVEA ENALGKVTSDHINFDPVYKV KPNPPHNLSVINSEELSSIL

       250        260        270        280        290        300
         *          *          *          *          *          *
KLTWTNPSIKSVIILKYNIQ YRTKDASTWSQIPPEDTAST RSSFTVQDLKPFTEYVFRIR

       310        320        330
         *          *          *
CMKEDGKGYWSDWSEEASGI TYEDRPSKAPSG
```

Fig.11.

Amino acid sequence of J-CH1

Sequence Range: 1 to 121

```
        10         20         30         40         50         60
         *          *          *          *          *          *
SGGQGTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTS

        70         80         90        100        110        120
         *          *          *          *          *          *
GVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHT*
```

Fig.12.

Amino acid sequence of Cγ4

Sequence Range: 1 to 330

```
        10         20         30         40         50         60
         *          *          *          *          *          *
SGASTKGPSVFPLAPCSRST SESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQ

        70         80         90        100        110        120
         *          *          *          *          *          *
SSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRV ESKYGPPCPSCPAPEFLGGP

       130        140        150        160        170        180
         *          *          *          *          *          *
SVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWY VDGVEVHNAKTKPREEQFNS

       190        200        210        220        230        240
         *          *          *          *          *          *
TYRVVSVLTVLHQDWLNGKE YKCKVSNKGLPSSIEKTISK AKGQPREPQVYTLPPSQEEM

       250        260        270        280        290        300
         *          *          *          *          *          *
TKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVL DSDGSFFLYSRLTVDKSRWQ

       310        320        330
         *          *          *
EGNVFSCSVMHEALHNHYTQ KSLSLSLGK*
```

Fig.13.

Amino acid sequence of κ-domain

Sequence Range: 1 to 108

```
         10          20          30          40          50          60
          *           *           *           *           *           *
SGTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKV QWKVDNALQSGNSQESVTEQ

         70          80          90         100
          *           *           *           *
DSKDSTYSLSSTLTLSKADY EKHKVYACEVTHQGLSSPVT KSFNRGEC*
```

Fig.14.

Amino acid sequence of λ-domain:

Sequence Range: 1 to 107

```
         10          20          30          40          50          60
          *           *           *           *           *           *
SGPKAAPSVTLFPPSSEELQ ANKATLVCLISDFYPGAVTV AWKADSSPVKAGVETTTPSK

         70          80          90         100
          *           *           *           *
QSNNKYAASSYLSLTPEQWK SHRSYSCQVTHEGSTVEKTV APTECS*
```

Fig.15.

Amino acid sequence of the soluble IL-6Rα domain

Sequence Range: 1 to 360

```
        10         20         30         40         50         60
         *          *          *          *          *          *
MVAVGCALLAALLAAPGAAL APRRCPAQEVARGVLTSLPG DSVTLTCPGVEPEDNATVHW

        70         80         90        100        110        120
         *          *          *          *          *          *
VLRKPAAGSHPSRWAGMGRR LLLRSVQLHDSGNYSCYRAG RPAGTVHLLVDVPPEEPQLS

       130        140        150        160        170        180
         *          *          *          *          *          *
CFRKSPLSNVVCEWGPRSTP SLTTKAVLLVRKFQNSPAED FQEPCQYSQESQKFSCQLAV

       190        200        210        220        230        240
         *          *          *          *          *          *
PEGDSSFYIVSMCVASSVGS KFSKTQTFQGCGILQPDPPA NITVTAVARNPRWLSVTWQD

       250        260        270        280        290        300
         *          *          *          *          *          *
PHSWNSSFYRLRFELRYRAE RSKTFTTWMVKDLQHHCVIH DAWSGLRHVVQLRAQEEFGQ

       310        320        330        340        350        360
         *          *          *          *          *          *
GEWSEWSPEAMGTPWTESRS PPAENEVSTPMQALTTNKDD DNILFRDSANATSLPVQDAG
```

Fig.16.

Amino acid sequence of the soluble IL-6Kα313 domain

Sequence Range: 1 to 315

```
        10         20         30         40         50         60
         *          *          *          *          *          *
MVAVGCALLAALLAAPGAAL APRRCPAQEVARGVLTSLPG DSVTLTCPGVEPEDNATVHW

        70         80         90        100        110        120
         *          *          *          *          *          *
VLRKPAAGSHPSRWAGMGRR LLLRSVQLHDSGNYSCYRAG RPAGTVHLLVDVPPEEPQLS

       130        140        150        160        170        180
         *          *          *          *          *          *
CFRKSPLSNVVCEWGPRSTP SLTTKAVLLVRKFQNSPAED FQEPCQYSQESQKFSCQLAV

       190        200        210        220        230        240
         *          *          *          *          *          *
PEGDSSFYIVSMCVASSVGS KFSKTQTFQGCGILQPDPPA NITVTAVARNPRWLSVTWQD

       250        260        270        280        290        300
         *          *          *          *          *          *
PHSWNSSFYRLRFELRYRAE RSKTFTTWMVKDLQHHCVIH DAWSGLRHVVQLRAQEEFGQ

       310
         *
GEWSEWSPEAMGTTG
```

Fig.17.

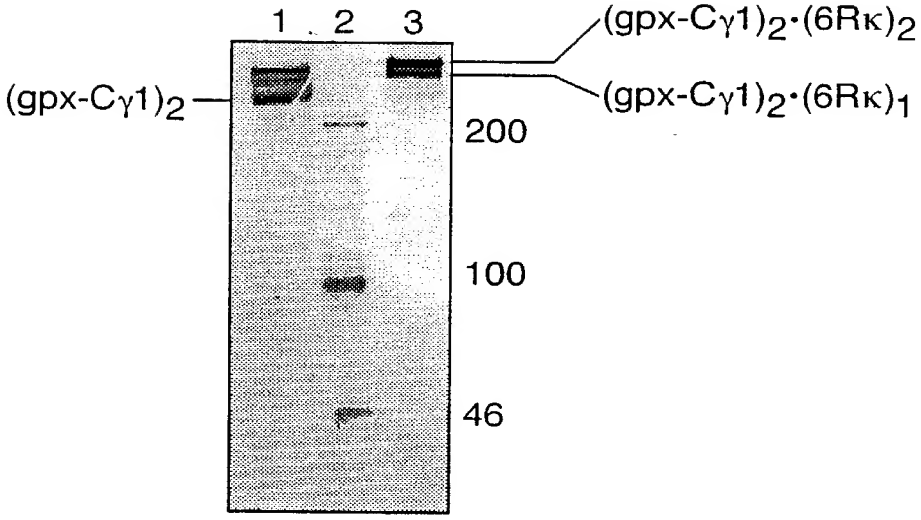
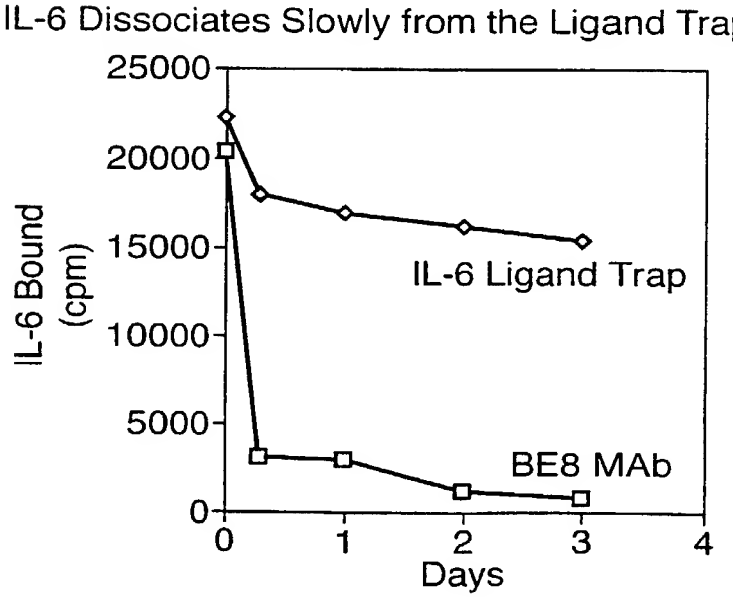

1
2
3
(gpx-Cγ1)2·(6Rκ)2
(gpx-Cγ1)2
(gpx-Cγ1)2·(6Rκ)1
200
100
46

Fig.18.


IL-6 Dissociates Slowly from the Ligand Trap
25000
20000
15000
10000
5000
0
IL-6 Bound (cpm)
IL-6 Ligand Trap
BE8 MAb
0
1
2
3
4
Days

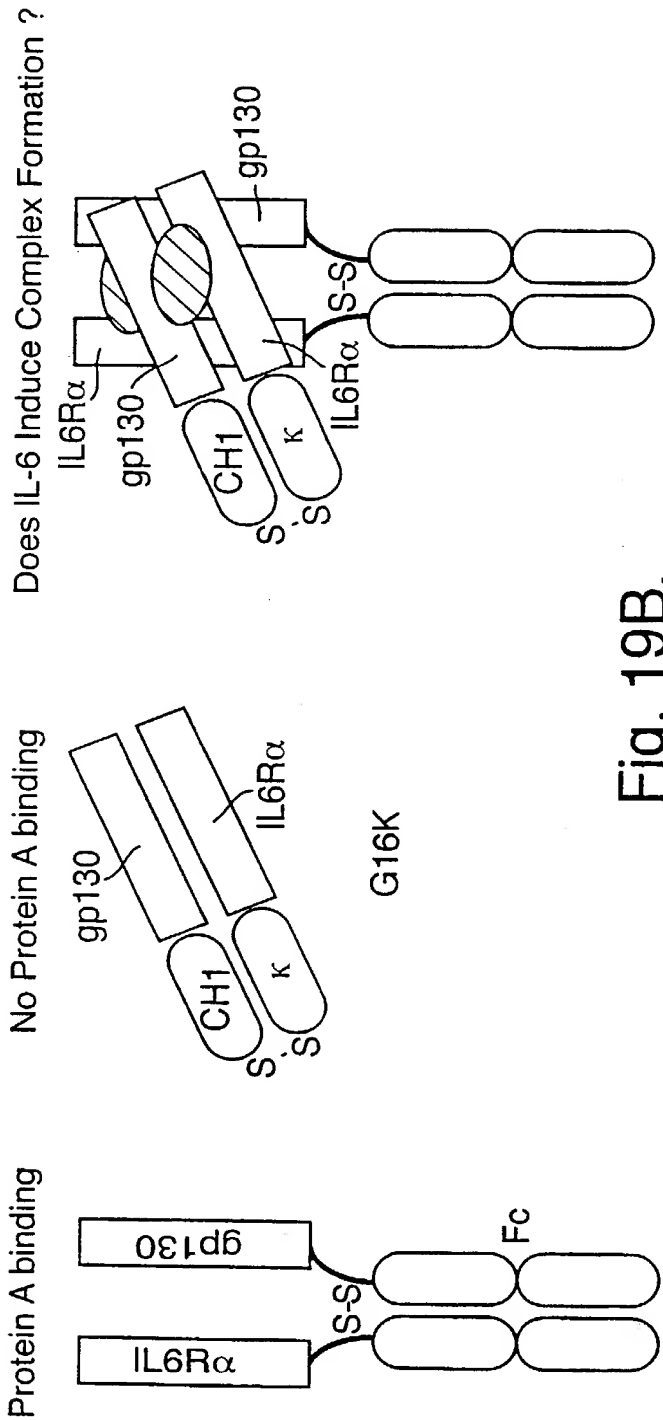


Fig. 19A.
Does IL-6 Induce Complex Formation ?
IL6Rα
gp130
gp130
IL6Rα
S-S
CH1
κ
S
S
No Protein A binding
gp130
IL6Rα
G16K
CH1
κ
S
S
Protein A binding
gp130
IL6Rα
S-S
Fc
GF6F

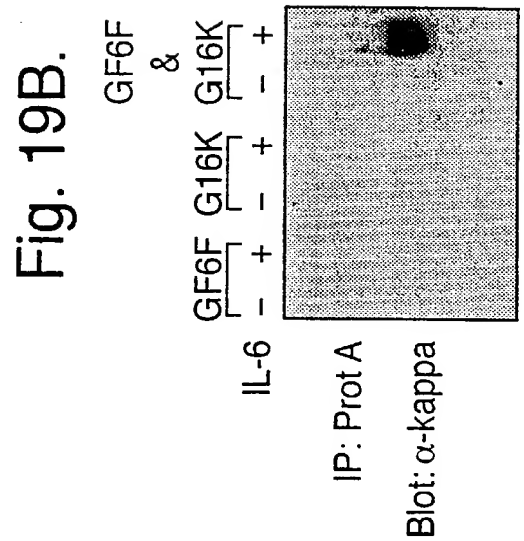


Fig. 19B.
GF6F
&
G16K
GF6F
G16K
IL-6
– + – + – +
IP: Prot A
Blot: α-kappa

Fig.20.

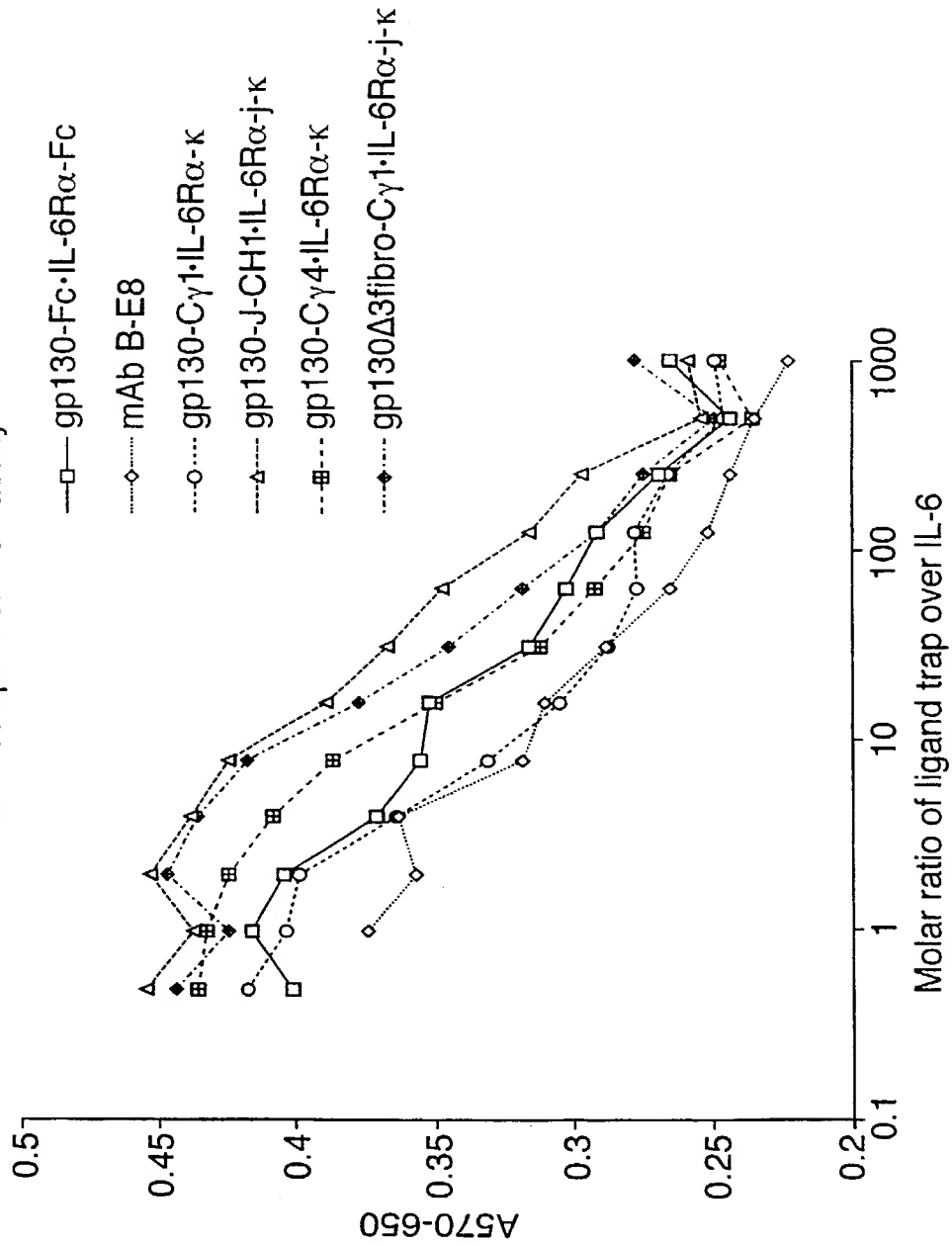

XG-1 cell proliferation assay
gp130-Fc·IL-6Rα-Fc
mAb B-E8
gp130-Cγ1·IL-6Rα-κ
gp130-J-CH1·IL-6Rα-j-κ
gp130-Cγ4·IL-6Rα-κ
gp130Δ3fibro-Cγ1·IL-6Rα-j-κ
A570-650
0.5
0.45
0.4
0.35
0.3
0.25
0.2
0.1
1
10
100
1000
Molar ratio of ligand trap over IL-6

Fig.21A.


```
          10          20          30          40
     *    *    *    *    *    *    *    *    *
ATG GTG AAG CCA TCA TTA CCA TTC ACA TCC CTC TTA TTC CTG CAG CTG
Met Val Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu>

50          60          70          80          90
 *    *    *    *    *    *    *    *    *    *
CCC CTG CTG GGA GTG GGG CTG AAC ACG ACA ATT CTG ACG CCC AAT GGG
Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly>

  100         110         120         130         140
    *    *    *    *    *    *    *    *    *
AAT GAA GAC ACC ACA GCT GAT TTC TTC CTG ACC ACT ATG CCC ACT GAC
Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp>

    150         160         170         180         190
*    *    *    *    *    *    *    *    *    *
TCC CTC AGT GTT TCC ACT CTG CCC CTC CCA GAG GTT CAG TGT TTT GTG
Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val>

        200         210         220         230         240
  *    *    *    *    *    *    *    *    *    *
TTC AAT GTC GAG TAC ATG AAT TGC ACT TGG AAC AGC AGC TCT GAG CCC
Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro>

          250         260         270         280
     *    *    *    *    *    *    *    *    *
CAG CCT ACC AAC CTC ACT CTG CAT TAT TGG TAC AAG AAC TCG GAT AAT
Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn>

290         300         310         320         330
  *    *    *    *    *    *    *    *    *    *
GAT AAA GTC CAG AAG TGC AGC CAC TAT CTA TTC TCT GAA GAA ATC ACT
Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr>

  340         350         360         370         380
    *    *    *    *    *    *    *    *    *
TCT GGC TGT CAG TTG CAA AAA AAG GAG ATC CAC CTC TAC CAA ACA TTT
Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe>

    390         400         410         420         430
*    *    *    *    *    *    *    *    *    *
GTT GTT CAG CTC CAG GAC CCA CGG GAA CCC AGG AGA CAG GCC ACA CAG
Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln>

        440         450         460         470         480
  *    *    *    *    *    *    *    *    *    *
ATG CTA AAA CTG CAG AAT CTG GTG ATC CCC TGG GCT CCA GAG AAC CTA
Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu>

          490         500         510         520
     *    *    *    *    *    *    *    *    *
ACA CTT CAC AAA CTG AGT GAA TCC CAG CTA GAA CTG AAC TGG AAC AAC
Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn>

530         540         550         560         570
  *    *    *    *    *    *    *    *    *    *
AGA TTC TTG AAC CAC TGT TTG GAG CAC TTG GTG CAG TAC CGG ACT GAC
Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp>
```

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Fig.21B.


```
   580          590          600          610          620
    *    *       *    *       *    *       *    *       *
TGG GAC CAC AGC TGG ACT GAA CAA TCA GTG GAT TAT AGA CAT AAG TTC
Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe>

     630          640          650          660          670
*    *       *    *       *    *       *    *       *    *
TCC TTG CCT AGT GTG GAT GGG CAG AAA CGC TAC ACG TTT CGT GTT CGG
Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg>

       680          690          700          710          720
 *     *    *       *    *       *    *       *    *       *
AGC CGC TTT AAC CCA CTC TGT GGA AGT GCT CAG CAT TGG AGT GAA TGG
Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp>

          730          740          750          760
    *     *    *       *    *       *    *       *    *
AGC CAC CCA ATC CAC TGG GGG AGC AAT ACT TCA AAA GAG AAC GCG TCG
Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Ala Ser>

770          780          790          800          810
 *    *       *    *       *    *       *    *       *    *
TCT GGG AAC ATG AAG GTC CTG CAG GAG CCC ACC TGC GTC TCC GAC TAC
Ser Gly Asn Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr>

   820          830          840          850          860
    *    *       *    *       *    *       *    *       *
ATG AGC ATC TCT ACT TGC GAG TGG AAG ATG AAT GGT CCC ACC AAT TGC
Met Ser Ile Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys>

     870          880          890          900          910
*    *       *    *       *    *       *    *       *    *
AGC ACC GAG CTC CGC CTG TTG TAC CAG CTG GTT TTT CTG CTC TCC GAA
Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu>

       920          930          940          950          960
 *     *    *       *    *       *    *       *    *       *
GCC CAC ACG TGT ATC CCT GAG AAC AAC GGA GGC GCG GGG TGC GTG TGC
Ala His Thr Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys>

          970          980          990         1000
    *     *    *       *    *       *    *       *    *
CAC CTG CTC ATG GAT GAC GTG GTC AGT GCG GAT AAC TAT ACA CTG GAC
His Leu Leu Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp>

1010         1020         1030         1040         1050
 *    *       *    *       *    *       *    *       *    *
CTG TGG GCT GGG CAG CAG CTG CTG TGG AAG GGC TCC TTC AAG CCC AGC
Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser>

  1060         1070         1080         1090         1100
    *    *       *    *       *    *       *    *       *
GAG CAT GTG AAA CCC AGG GCC CCA GGA AAC CTG ACA GTT CAC ACC AAT
Glu His Val Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn>

    1110         1120         1130         1140         1150
*    *       *    *       *    *       *    *       *    *
GTC TCC GAC ACT CTG CTG CTG ACC TGG AGC AAC CCG TAT CCC CCT GAC
Val Ser Asp Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp>

        1160         1170         1180         1190         1200
 *      *    *       *    *       *    *       *    *       *
```

Fig.21C.

```
AAT TAC CTG TAT AAT CAT CTC ACC TAT GCA GTC AAC ATT TGG AGT GAA
Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu>

         1210         1220         1230         1240
      *    *    *    *    *    *    *    *    *    *
AAC GAC CCG GCA GAT TTC AGA ATC TAT AAC GTG ACC TAC CTA GAA CCC
Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro>

1250         1260         1270         1280         1290
  *    *    *    *    *    *    *    *    *    *    *    *
TCC CTC CGC ATC GCA GCC AGC ACC CTG AAG TCT GGG ATT TCC TAC AGG
Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg>

 1300         1310         1320         1330         1340
    *    *    *    *    *    *    *    *    *    *
GCA CGG GTG AGG GCC TGG GCT CAG TGC TAT AAC ACC ACC TGG AGT GAG
Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr Asn Thr Thr Trp Ser Glu>

   1350         1360         1370         1380         1390
 *    *    *    *    *    *    *    *    *    *    *    *
TGG AGC CCC AGC ACC AAG TGG CAC AAC TCC TAC AGG GAG CCC TTC GAG
Trp Ser Pro Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu>

      1400         1410         1420         1430         1440
   *    *    *    *    *    *    *    *    *    *    *    *
CAG TCC GGA GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA
Gln Ser Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu>

         1450         1460         1470         1480
      *    *    *    *    *    *    *    *    *    *
CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp>

1490         1500         1510         1520         1530
  *    *    *    *    *    *    *    *    *    *    *    *
ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp>

 1540         1550         1560         1570         1580
    *    *    *    *    *    *    *    *    *    *
GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly>

   1590         1600         1610         1620         1630
 *    *    *    *    *    *    *    *    *    *    *    *
GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn>

      1640         1650         1660         1670         1680
   *    *    *    *    *    *    *    *    *    *    *    *
AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp>

         1690         1700         1710         1720
      *    *    *    *    *    *    *    *    *    *
CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro>

1730         1740         1750         1760         1770
  *    *    *    *    *    *    *    *    *    *    *    *
GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu>
```

Fig.21D.

```
 1780          1790          1800          1810          1820
    *     *       *     *     *       *     *     *       *
CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAG GAG ATG ACC AAG AAC
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn>

   1830          1840          1850          1860          1870
*     *       *     *     *       *     *     *       *       *
CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile>

      1880          1890          1900          1910          1920
  *       *     *       *     *       *     *       *     *       *
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr>

         1930          1940          1950          1960
     *       *     *       *     *       *     *       *     *
ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAT AGC AAG
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys>

1970          1980          1990          2000          2010
  *       *     *       *     *       *     *       *     *       *
CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys>

 2020          2030          2040          2050          2060
    *     *       *     *     *       *     *     *       *
TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu>

   2070          2080
*     *       *     *     *
TCC CTG TCT CCG GGT AAA TGA
Ser Leu Ser Pro Gly Lys ***>
```

Fig.22A.


```
          10          20          30          40
     *    *    *    *    *    *    *    *    *
ATG GTG AAG CCA TCA TTA CCA TTC ACA TCC CTC TTA TTC CTG CAG CTG
Met Val Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu>

50          60          70          80          90
 *    *    *    *    *    *    *    *    *    *
CCC CTG CTG GGA GTG GGG CTG AAC ACG ACA ATT CTG ACG CCC AAT GGG
Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly>

  100         110         120         130         140
    *    *    *    *    *    *    *    *    *
AAT GAA GAC ACC ACA GCT GAT TTC TTC CTG ACC ACT ATG CCC ACT GAC
Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp>

    150         160         170         180         190
*    *    *    *    *    *    *    *    *    *
TCC CTC AGT GTT TCC ACT CTG CCC CTC CCA GAG GTT CAG TGT TTT GTG
Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val>

       200         210         220         230         240
  *    *    *    *    *    *    *    *    *    *    *    *
TTC AAT GTC GAG TAC ATG AAT TGC ACT TGG AAC AGC AGC TCT GAG CCC
Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro>

          250         260         270         280
     *    *    *    *    *    *    *    *    *
CAG CCT ACC AAC CTC ACT CTG CAT TAT TGG TAC AAG AAC TCG GAT AAT
Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn>

290         300         310         320         330
 *    *    *    *    *    *    *    *    *    *
GAT AAA GTC CAG AAG TGC AGC CAC TAT CTA TTC TCT GAA GAA ATC ACT
Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr>

  340         350         360         370         380
    *    *    *    *    *    *    *    *    *
TCT GGC TGT CAG TTG CAA AAA AAG GAG ATC CAC CTC TAC CAA ACA TTT
Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe>

    390         400         410         420         430
*    *    *    *    *    *    *    *    *    *
GTT GTT CAG CTC CAG GAC CCA CGG GAA CCC AGG AGA CAG GCC ACA CAG
Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln>

       440         450         460         470         480
  *    *    *    *    *    *    *    *    *    *    *    *
ATG CTA AAA CTG CAG AAT CTG GTG ATC CCC TGG GCT CCA GAG AAC CTA
Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu>

          490         500         510         520
     *    *    *    *    *    *    *    *    *
ACA CTT CAC AAA CTG AGT GAA TCC CAG CTA GAA CTG AAC TGG AAC AAC
Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn>

530         540         550         560         570
 *    *    *    *    *    *    *    *    *    *
AGA TTC TTG AAC CAC TGT TTG GAG CAC TTG GTG CAG TAC CGG ACT GAC
Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp>
```

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Fig.22B.


```
   580          590          600          610          620
    *    *       *    *       *    *       *    *       *
TGG GAC CAC AGC TGG ACT GAA CAA TCA GTG GAT TAT AGA CAT AAG TTC
Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe>

    630          640          650          660          670
*    *       *    *       *    *       *    *       *    *
TCC TTG CCT AGT GTG GAT GGG CAG AAA CGC TAC ACG TTT CGT GTT CGG
Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg>

        680          690          700          710          720
  *    *       *    *       *    *       *    *       *    *
AGC CGC TTT AAC CCA CTC TGT GGA AGT GCT CAG CAT TGG AGT GAA TGG
Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp>

          730          740          750          760
     *    *       *    *       *    *       *    *    *
AGC CAC CCA ATC CAC TGG GGG AGC AAT ACT TCA AAA GAG AAC GGG AAC
Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Gly Asn>

770          780          790          800          810
  *    *       *    *       *    *       *    *       *
ATG AAG GTC CTG CAG GAG CCC ACC TGC GTC TCC GAC TAC ATG AGC ATC
Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr Met Ser Ile>

   820          830          840          850          860
    *    *       *    *       *    *       *    *       *
TCT ACT TGC GAG TGG AAG ATG AAT GGT CCC ACC AAT TGC AGC ACC GAG
Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys Ser Thr Glu>

    870          880          890          900          910
*    *       *    *       *    *       *    *       *    *
CTC CGC CTG TTG TAC CAG CTG GTT TTT CTG CTC TCC GAA GCC CAC ACG
Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu Ala His Thr>

        920          930          940          950          960
  *    *       *    *       *    *       *    *       *    *
TGT ATC CCT GAG AAC AAC GGA GGC GCG GGG TGC GTG TGC CAC CTG CTC
Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys His Leu Leu>

          970          980          990          1000
     *    *       *    *       *    *       *    *    *
ATG GAT GAC GTG GTC AGT GCG GAT AAC TAT ACA CTG GAC CTG TGG GCT
Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp Leu Trp Ala>

1010         1020         1030         1040         1050
  *    *       *    *       *    *       *    *       *
GGG CAG CAG CTG CTG TGG AAG GGC TCC TTC AAG CCC AGC GAG CAT GTG
Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser Glu His Val>

 1060         1070         1080         1090         1100
    *    *       *    *       *    *       *    *       *
AAA CCC AGG GCC CCA GGA AAC CTG ACA GTT CAC ACC AAT GTC TCC GAC
Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn Val Ser Asp>

   1110         1120         1130         1140         1150
*    *       *    *       *    *       *    *       *    *
ACT CTG CTG CTG ACC TGG AGC AAC CCG TAT CCC CCT GAC AAT TAC CTG
Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp Asn Tyr Leu>

        1160         1170         1180         1190         1200
  *    *       *    *       *    *       *    *       *    *
```

Fig.22C.


```
TAT AAT CAT CTC ACC TAT GCA GTC AAC ATT TGG AGT GAA AAC GAC CCG
Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu Asn Asp Pro>

        1210         1220         1230         1240
      *    *    *    *    *    *    *    *    *
GCA GAT TTC AGA ATC TAT AAC GTG ACC TAC CTA GAA CCC TCC CTC CGC
Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro Ser Leu Arg>

1250         1260         1270         1280         1290
  *    *    *    *    *    *    *    *    *    *
ATC GCA GCC AGC ACC CTG AAG TCT GGG ATT TCC TAC AGG GCA CGG GTG
Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg Ala Arg Val>

 1300         1310         1320         1330         1340
    *    *    *    *    *    *    *    *    *
AGG GCC TGG GCT CAG AGC TAT AAC ACC ACC TGG AGT GAG TGG AGC CCC
Arg Ala Trp Ala Gln Ser Tyr Asn Thr Thr Trp Ser Glu Trp Ser Pro>

   1350         1360         1370         1380         1390
 *    *    *    *    *    *    *    *    *    *
AGC ACC AAG TGG CAC AAC TCC TAC AGG GAG CCC TTC GAG CAG TCC GGA
Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu Gln Ser Gly>

      1400         1410         1420         1430         1440
   *    *    *    *    *    *    *    *    *    *
GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly>

        1450         1460         1470         1480
      *    *    *    *    *    *    *    *    *
GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met>

1490         1500         1510         1520         1530
  *    *    *    *    *    *    *    *    *    *
ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His>

 1540         1550         1560         1570         1580
    *    *    *    *    *    *    *    *    *
GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val>

   1590         1600         1610         1620         1630
 *    *    *    *    *    *    *    *    *    *
CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr>

      1640         1650         1660         1670         1680
   *    *    *    *    *    *    *    *    *    *
CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly>

        1690         1700         1710         1720
      *    *    *    *    *    *    *    *    *
AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile>

1730         1740         1750         1760         1770
  *    *    *    *    *    *    *    *    *    *
GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val>
```

Fig.22D.

```
 1780          1790          1800          1810          1820
    *     *       *     *       *     *       *     *       *
TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser>

   1830          1840          1850          1860          1870
*     *       *     *       *     *       *     *       *     *
CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu>

      1880          1890          1900          1910          1920
  *       *     *       *     *       *     *       *     *       *
TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro>

         1930          1940          1950          1960
     *       *     *       *     *       *     *       *
GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAT AGC AAG CTC ACC GTG
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val>

1970          1980          1990          2000          2010
   *     *       *     *       *     *       *     *       *
GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met>

 2020          2030          2040          2050          2060
    *     *       *     *       *     *       *     *       *
CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser>

   2070
*     *       *
CCG GGT AAA TGA
Pro Gly Lys ***>
```

Fig.23A.

```
          10          20          30          40
      *   *   *   *   *   *   *   *   *   *
ATG GTG AAG CCA TCA TTA CCA TTC ACA TCC CTC TTA TTC CTG CAG CTG
Met Val Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu>

50          60          70          80          90
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CCC CTG CTG GGA GTG GGG CTG AAC ACG ACA ATT CTG ACG CCC AAT GGG
Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly>

  100         110         120         130         140
   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AAT GAA GAC ACC ACA GCT GAT TTC TTC CTG ACC ACT ATG CCC ACT GAC
Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp>

    150         160         170         180         190
*   *   *   *   *   *   *   *   *   *   *   *   *   *   *
TCC CTC AGT GTT TCC ACT CTG CCC CTC CCA GAG GTT CAG TGT TTT GTG
Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val>

       200         210         220         230         240
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
TTC AAT GTC GAG TAC ATG AAT TGC ACT TGG AAC AGC AGC TCT GAG CCC
Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro>

          250         260         270         280
      *   *   *   *   *   *   *   *   *   *
CAG CCT ACC AAC CTC ACT CTG CAT TAT TGG TAC AAG AAC TCG GAT AAT
Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn>

290         300         310         320         330
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GAT AAA GTC CAG AAG TGC AGC CAC TAT CTA TTC TCT GAA GAA ATC ACT
Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr>

  340         350         360         370         380
   *   *   *   *   *   *   *   *   *   *   *   *   *   *
TCT GGC TGT CAG TTG CAA AAA AAG GAG ATC CAC CTC TAC CAA ACA TTT
Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe>

    390         400         410         420         430
*   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GTT GTT CAG CTC CAG GAC CCA CGG GAA CCC AGG AGA CAG GCC ACA CAG
Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln>

       440         450         460         470         480
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
ATG CTA AAA CTG CAG AAT CTG GTG ATC CCC TGG GCT CCA GAG AAC CTA
Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu>

          490         500         510         520
      *   *   *   *   *   *   *   *   *   *
ACA CTT CAC AAA CTG AGT GAA TCC CAG CTA GAA CTG AAC TGG AAC AAC
Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn>

530         540         550         560         570
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AGA TTC TTG AAC CAC TGT TTG GAG CAC TTG GTG CAG TAC CGG ACT GAC
Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp>
```

Fig.23B.


```
   580          590          600          610          620
    *    *       *    *       *    *       *    *       *
TGG GAC CAC AGC TGG ACT GAA CAA TCA GTG GAT TAT AGA CAT AAG TTC
Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe>

     630          640          650          660          670
*    *       *    *       *    *       *    *       *    *
TCC TTG CCT AGT GTG GAT GGG CAG AAA CGC TAC ACG TTT CGT GTT CGG
Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg>

       680          690          700          710          720
  *    *       *    *       *    *       *    *       *    *
AGC CGC TTT AAC CCA CTC TGT GGA AGT GCT CAG CAT TGG AGT GAA TGG
Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp>

          730          740          750          760
     *    *       *    *       *    *       *    *
AGC CAC CCA ATC CAC TGG GGG AGC AAT ACT TCA AAA GAG AAC GCG TCG
Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Ala Ser>

770          780          790          800          810
  *    *       *    *       *    *       *    *       *
TCT GGG AAC ATG AAG GTC CTG CAG GAG CCC ACC TGC GTC TCC GAC TAC
Ser Gly Asn Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr>

   820          830          840          850          860
    *    *       *    *       *    *       *    *       *
ATG AGC ATC TCT ACT TGC GAG TGG AAG ATG AAT GGT CCC ACC AAT TGC
Met Ser Ile Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys>

     870          880          890          900          910
*    *       *    *       *    *       *    *       *    *
AGC ACC GAG CTC CGC CTG TTG TAC CAG CTG GTT TTT CTG CTC TCC GAA
Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu>

       920          930          940          950          960
  *    *       *    *       *    *       *    *       *    *
GCC CAC ACG TGT ATC CCT GAG AAC AAC GGA GGC GCG GGG TGC GTG TGC
Ala His Thr Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys>

          970          980          990          1000
     *    *       *    *       *    *       *    *
CAC CTG CTC ATG GAT GAC GTG GTC AGT GCG GAT AAC TAT ACA CTG GAC
His Leu Leu Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp>

1010         1020         1030         1040         1050
  *    *       *    *       *    *       *    *       *
CTG TGG GCT GGG CAG CAG CTG CTG TGG AAG GGC TCC TTC AAG CCC AGC
Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser>

  1060         1070         1080         1090         1100
    *    *       *    *       *    *       *    *       *
GAG CAT GTG AAA CCC AGG GCC CCA GGA AAC CTG ACA GTT CAC ACC AAT
Glu His Val Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn>

   1110         1120         1130         1140         1150
*    *       *    *       *    *       *    *       *    *
GTC TCC GAC ACT CTG CTG CTG ACC TGG AGC AAC CCG TAT CCC CCT GAC
Val Ser Asp Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp>

       1160         1170         1180         1190         1200
  *    *       *    *       *    *       *    *       *    *
```

Fig.23C.


```
AAT TAC CTG TAT AAT CAT CTC ACC TAT GCA GTC AAC ATT TGG AGT GAA
Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu>

         1210         1220         1230         1240
       *    *    *    *    *    *    *    *    *    *
AAC GAC CCG GCA GAT TTC AGA ATC TAT AAC GTG ACC TAC CTA GAA CCC
Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro>

1250         1260         1270         1280         1290
   *    *    *    *    *    *    *    *    *    *    *
TCC CTC CGC ATC GCA GCC AGC ACC CTG AAG TCT GGG ATT TCC TAC AGG
Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg>

 1300         1310         1320         1330         1340
    *    *    *    *    *    *    *    *    *    *
GCA CGG GTG AGG GCC TGG GCT CAG AGC TAT AAC ACC ACC TGG AGT GAG
Ala Arg Val Arg Ala Trp Ala Gln Ser Tyr Asn Thr Thr Trp Ser Glu>

   1350         1360         1370         1380         1390
*    *    *    *    *    *    *    *    *    *    *
TGG AGC CCC AGC ACC AAG TGG CAC AAC TCC TAC AGG GAG CCC TTC GAG
Trp Ser Pro Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu>

      1400         1410         1420         1430         1440
  *    *    *    *    *    *    *    *    *    *    *
CAG TCC GGA GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA
Gln Ser Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu>

         1450         1460         1470         1480
       *    *    *    *    *    *    *    *    *
CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp>

1490         1500         1510         1520         1530
   *    *    *    *    *    *    *    *    *    *
ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp>

 1540         1550         1560         1570         1580
    *    *    *    *    *    *    *    *    *    *
GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly>

   1590         1600         1610         1620         1630
*    *    *    *    *    *    *    *    *    *    *
GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn>

      1640         1650         1660         1670         1680
  *    *    *    *    *    *    *    *    *    *    *
AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp>

         1690         1700         1710         1720
       *    *    *    *    *    *    *    *    *
CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro>

1730         1740         1750         1760         1770
   *    *    *    *    *    *    *    *    *    *
GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu>
```

Fig.23D.

```
 1780          1790          1800          1810          1820
    *     *       *     *       *     *       *     *       *
CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn>

   1830          1840          1850          1860          1870
*     *       *     *       *     *       *     *       *     *
CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile>

      1880          1890          1900          1910          1920
  *     *       *     *       *     *       *     *       *     *
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr>

         1930          1940          1950          1960
     *     *       *     *       *     *       *     *     *
ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAT AGC AAG
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys>

1970          1980          1990          2000          2010
   *     *       *     *       *     *       *     *       *     *
CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys>

 2020          2030          2040          2050          2060
    *     *       *     *       *     *       *     *       *
TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu>

   2070          2080
*     *       *     *     *
TCC CTG TCT CCG GGT AAA TGA
Ser Leu Ser Pro Gly Lys ***>
```

Fig.24A.

```
          10          20          30          40
      *   *   *   *   *   *   *   *   *   *
ATG GTG GCC GTC GGC TGC GCG CTG CTG GCT GCC CTG CTG GCC GCG CCG
Met Val Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro>

50          60          70          80          90
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GGA GCG GCG CTG GCC CCA AGG CGC TGC CCT GCG CAG GAG GTG GCA AGA
Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg>

  100         110         120         130         140
   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GGC GTG CTG ACC AGT CTG CCA GGA GAC AGC GTG ACT CTG ACC TGC CCG
Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro>

    150         160         170         180         190
*   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GGG GTA GAG CCG GAA GAC AAT GCC ACT GTT CAC TGG GTG CTC AGG AAG
Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys>

      200         210         220         230         240
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CCG GCT GCA GGC TCC CAC CCC AGC AGA TGG GCT GGC ATG GGA AGG AGG
Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg>

          250         260         270         280
      *   *   *   *   *   *   *   *   *   *   *
CTG CTG CTG AGG TCG GTG CAG CTC CAC GAC TCT GGA AAC TAT TCA TGC
Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys>

290         300         310         320         330
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
TAC CGG GCC GGC CGC CCA GCT GGG ACT GTG CAC TTG CTG GTG GAT GTT
Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val>

  340         350         360         370         380
   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CCC CCC GAG GAG CCC CAG CTC TCC TGC TTC CGG AAG AGC CCC CTC AGC
Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser>

    390         400         410         420         430
*   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AAT GTT GTT TGT GAG TGG GGT CCT CGG AGC ACC CCA TCC CTG ACG ACA
Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr>

      440         450         460         470         480
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AAG GCT GTG CTC TTG GTG AGG AAG TTT CAG AAC AGT CCG GCC GAA GAC
Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp>

          490         500         510         520
      *   *   *   *   *   *   *   *   *   *   *
TTC CAG GAG CCG TGC CAG TAT TCC CAG GAG TCC CAG AAG TTC TCC TGC
Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys>

530         540         550         560         570
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CAG TTA GCA GTC CCG GAG GGA GAC AGC TCT TTC TAC ATA GTG TCC ATG
Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met>
```

Fig.24B.


```
   580          590          600          610          620
     *    *       *    *       *    *       *    *       *
TGC GTC GCC AGT AGT GTC GGG AGC AAG TTC AGC AAA ACT CAA ACC TTT
Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe>

     630          640          650          660          670
*    *       *    *       *    *       *    *       *    *
CAG GGT TGT GGA ATC TTG CAG CCT GAT CCG CCT GCC AAC ATC ACA GTC
Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val>

       680          690          700          710          720
  *    *       *    *       *    *       *    *       *    *
ACT GCC GTG GCC AGA AAC CCC CGC TGG CTC AGT GTC ACC TGG CAA GAC
Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp>

          730          740          750          760
     *    *       *    *       *    *       *    *       *
CCC CAC TCC TGG AAC TCA TCT TTC TAC AGA CTA CGG TTT GAG CTC AGA
Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg>

770          780          790          800          810
  *    *       *    *       *    *       *    *       *    *
TAT CGG GCT GAA CGG TCA AAG ACA TTC ACA ACA TGG ATG GTC AAG GAC
Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp>

  820          830          840          850          860
    *    *       *    *       *    *       *    *       *
CTC CAG CAT CAC TGT GTC ATC CAC GAC GCC TGG AGC GGC CTG AGG CAC
Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His>

     870          880          890          900          910
*    *       *    *       *    *       *    *       *    *
GTG GTG CAG CTT CGT GCC CAG GAG GAG TTC GGG CAA GGC GAG TGG AGC
Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser>

       920          930          940          950          960
  *    *       *    *       *    *       *    *       *    *
GAG TGG AGC CCG GAG GCC ATG GGC ACG CCT TGG ACA GAA TCC AGG AGT
Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser>

          970          980          990          1000
     *    *       *    *       *    *       *    *       *
CCT CCA GCT GAG AAC GAG GTG TCC ACC CCC ATG ACC GGT GGC GCG CCT
Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Thr Gly Gly Ala Pro>

1010         1020         1030         1040         1050
  *    *       *    *       *    *       *    *       *    *
TCA GGT GCT CAG CTG GAA CTT CTA GAC CCA TGT GGT TAT ATC AGT CCT
Ser Gly Ala Gln Leu Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser Pro>

  1060         1070         1080         1090         1100
    *    *       *    *       *    *       *    *       *
GAA TCT CCA GTT GTA CAA CTT CAT TCT AAT TTC ACT GCA GTT TGT GTG
Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys Val>

    1110         1120         1130         1140         1150
*    *       *    *       *    *       *    *       *    *
CTA AAG GAA AAA TGT ATG GAT TAT TTT CAT GTA AAT GCT AAT TAC ATT
Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr Ile>

       1160         1170         1180         1190         1200
  *    *       *    *       *    *       *    *       *    *
```

Fig.24C.


```
GTC TGG AAA ACA AAC CAT TTT ACT ATT CCT AAG GAG CAA TAT ACT ATC
Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr Ile>

          1210         1220         1230         1240
      *    *    *    *    *    *    *    *    *    *
ATA AAC AGA ACA GCA TCC AGT GTC ACC TTT ACA GAT ATA GCT TCA TTA
Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser Leu>

1250         1260         1270         1280         1290
  *    *    *    *    *    *    *    *    *    *    *
AAT ATT CAG CTC ACT TGC AAC ATT CTT ACA TTC GGA CAG CTT GAA CAG
Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu Gln>

 1300         1310         1320         1330         1340
    *    *    *    *    *    *    *    *    *    *
AAT GTT TAT GGA ATC ACA ATA ATT TCA GGC TTG CCT CCA GAA AAA CCT
Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys Pro>

   1350         1360         1370         1380         1390
*    *    *    *    *    *    *    *    *    *    *
AAA AAT TTG AGT TGC ATT GTG AAC GAG GGG AAG AAA ATG AGG TGT GAG
Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys Glu>

      1400         1410         1420         1430         1440
  *    *    *    *    *    *    *    *    *    *    *    *
TGG GAT GGT GGA AGG GAA ACA CAC TTG GAG ACA AAC TTC ACT TTA AAA
Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu Lys>

          1450         1460         1470         1480
      *    *    *    *    *    *    *    *    *    *
TCT GAA TGG GCA ACA CAC AAG TTT GCT GAT TGC AAA GCA AAA CGT GAC
Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg Asp>

1490         1500         1510         1520         1530
  *    *    *    *    *    *    *    *    *    *    *
ACC CCC ACC TCA TGC ACT GTT GAT TAT TCT ACT GTG TAT TTT GTC AAC
Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val Asn>

 1540         1550         1560         1570         1580
    *    *    *    *    *    *    *    *    *    *
ATT GAA GTC TGG GTA GAA GCA GAG AAT GCC CTT GGG AAG GTT ACA TCA
Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr Ser>

   1590         1600         1610         1620         1630
*    *    *    *    *    *    *    *    *    *    *
GAT CAT ATC AAT TTT GAT CCT GTA TAT AAA GTG AAG CCC AAT CCG CCA
Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro Pro>

      1640         1650         1660         1670         1680
  *    *    *    *    *    *    *    *    *    *    *    *
CAT AAT TTA TCA GTG ATC AAC TCA GAG GAA CTG TCT AGT ATC TTA AAA
His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu Lys>

          1690         1700         1710         1720
      *    *    *    *    *    *    *    *    *    *
TTG ACA TGG ACC AAC CCA AGT ATT AAG AGT GTT ATA ATA CTA AAA TAT
Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys Tyr>

1730         1740         1750         1760         1770
  *    *    *    *    *    *    *    *    *    *    *
AAC ATT CAA TAT AGG ACC AAA GAT GCC TCA ACT TGG AGC CAG ATT CCT
Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile Pro>
```

Fig.24D.


```
1780        1790        1800        1810        1820
 *    *      *    *      *    *      *    *      *
CCT GAA GAC ACA GCA TCC ACC CGA TCT TCA TTC ACT GTC CAA GAC CTT
Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp Leu>

   1830        1840        1850        1860        1870
*    *      *    *      *    *      *    *      *    *
AAA CCT TTT ACA GAA TAT GTG TTT AGG ATT CGC TGT ATG AAG GAA GAT
Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu Asp>

      1880        1890        1900        1910        1920
  *    *      *    *      *    *      *    *      *    *
GGT AAG GGA TAC TGG AGT GAC TGG AGT GAA GAA GCA AGT GGG ATC ACC
Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile Thr>

         1930        1940        1950        1960
      *    *      *    *      *    *      *    *      *
TAT GAA GAT AGA CCA TCT AAA GCA CCA AGT TTC TGG TAT AAA ATA GAT
Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile Asp>

1970        1980        1990        2000        2010
 *    *      *    *      *    *      *    *      *    *
CCA TCC CAT ACT CAA GGC TAC AGA ACT GTA CAA CTC GTG TGG AAG ACA
Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln Leu Val Trp Lys Thr>

  2020        2030        2040        2050        2060
   *    *      *    *      *    *      *    *      *    *
TTG CCT CCT TTT GAA GCC AAT GGA AAA ATC TTG GAT TAT GAA GTG ACT
Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val Thr>

    2070        2080        2090        2100        2110
*    *      *    *      *    *      *    *      *    *
CTC ACA AGA TGG AAA TCA CAT TTA CAA AAT TAC ACA GTT AAT GCC ACA
Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Ala Thr>

       2120        2130        2140        2150        2160
   *    *      *    *      *    *      *    *      *    *
AAA CTG ACA GTA AAT CTC ACA AAT GAT CGC TAT CTA GCA ACC CTA ACA
Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu Thr>

         2170        2180        2190        2200
      *    *      *    *      *    *      *    *      *
GTA AGA AAT CTT GTT GGC AAA TCA GAT GCA GCT GTT TTA ACT ATC CCT
Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala Val Leu Thr Ile Pro>

2210        2220        2230        2240        2250
 *    *      *    *      *    *      *    *      *    *
GCC TGT GAC TTT CAA GCT ACT CAC CCT GTA ATG GAT CTT AAA GCA TTC
Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala Phe>

  2260        2270        2280        2290        2300
   *    *      *    *      *    *      *    *      *    *
CCC AAA GAT AAC ATG CTT TGG GTG GAA TGG ACT ACT CCA AGG GAA TCT
Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu Ser>

    2310        2320        2330        2340        2350
*    *      *    *      *    *      *    *      *    *
GTA AAG AAA TAT ATA CTT GAG TGG TGT GTG TTA TCA GAT AAA GCA CCC
Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala Pro>

       2360        2370        2380        2390        2400
```

Fig.24E.


```
   *       *       *       *       *       *       *       *       *       *
TGT ATC ACA GAC TGG CAA CAA GAA GAT GGT ACC GTG CAT CGC ACC TAT
Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr Tyr>

          2410          2420          2430          2440
      *       *       *       *       *       *       *       *
TTA AGA GGG AAC TTA GCA GAG AGC AAA TGC TAT TTG ATA ACA GTT ACT
Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val Thr>

2450          2460          2470          2480          2490
   *       *       *       *       *       *       *       *       *
CCA GTA TAT GCT GAT GGA CCA GGA AGC CCT GAA TCC ATA AAG GCA TAC
Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala Tyr>

 2500          2510          2520          2530          2540
    *       *       *       *       *       *       *       *       *
CTT AAA CAA GCT CCA CCT TCC AAA GGA CCT ACT GTT CGG ACA AAA AAA
Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys Lys>

    2550          2560          2570          2580          2590
  *       *       *       *       *       *       *       *       *       *
GTA GGG AAA AAC GAA GCT GTC TTA GAG TGG GAC CAA CTT CCT GTT GAT
Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val Asp>

       2600          2610          2620          2630          2640
   *       *       *       *       *       *       *       *       *       *
GTT CAG AAT GGA TTT ATC AGA AAT TAT ACT ATA TTT TAT AGA ACC ATC
Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr Ile>

          2650          2660          2670          2680
      *       *       *       *       *       *       *       *       *
ATT GGA AAT GAA ACT GCT GTG AAT GTG GAT TCT TCC CAC ACA GAA TAT
Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu Tyr>

2690          2700          2710          2720          2730
   *       *       *       *       *       *       *       *       *       *
ACA TTG TCC TCT TTG ACT AGT GAC ACA TTG TAC ATG GTA CGA ATG GCA
Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met Ala>

 2740          2750          2760          2770          2780
    *       *       *       *       *       *       *       *       *
GCA TAC ACA GAT GAA GGT GGG AAG GAT GGT CCA GAA TTC ACT TTT ACT
Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe Thr>

    2790          2800          2810          2820          2830
  *       *       *       *       *       *       *       *       *       *
ACC CCA AAG TTT GCT CAA GGA GAA ATT GAA TCC GGG GGC GAC AAA ACT
Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ser Gly Gly Asp Lys Thr>

       2840          2850          2860          2870          2880
   *       *       *       *       *       *       *       *       *       *
CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser>

          2890          2900          2910          2920
      *       *       *       *       *       *       *       *       *
GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg>

2930          2940          2950          2960          2970
   *       *       *       *       *       *       *       *       *       *
ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT
```

Fig.24F.

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Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro>

 2980         2990         3000         3010         3020
    *    *       *    *       *    *       *    *       *
GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala>

   3030         3040         3050         3060         3070
*     *      *     *      *     *      *     *      *     *
AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val>

       3080         3090         3100         3110         3120
  *      *     *      *     *      *     *      *     *      *
AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr>

          3130         3140         3150         3160
     *      *     *      *     *      *     *      *     *
AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr>

3170         3180         3190         3200         3210
   *      *     *      *     *      *     *      *     *
ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu>

 3220         3230         3240         3250         3260
    *    *       *    *       *    *       *    *       *
CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys>

   3270         3280         3290         3300         3310
*     *      *     *      *     *      *     *      *     *
CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser>

       3320         3330         3340         3350         3360
  *      *     *      *     *      *     *      *     *      *
AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp>

          3370         3380         3390         3400
     *      *     *      *     *      *     *      *     *
TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser>

3410         3420         3430         3440         3450
   *      *     *      *     *      *     *      *     *
AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala>

 3460         3470         3480         3490         3500
    *    *       *    *       *    *       *    *       *
CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys>

*
TGA
***>
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Fig.25A.

```
          10          20          30          40
      *   *   *   *   *   *   *   *   *   *
ATG GTG GCC GTC GGC TGC GCG CTG CTG GCT GCC CTG CTG GCC GCG CCG
Met Val Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro>

50          60          70          80          90
 *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GGA GCG GCG CTG GCC CCA AGG CGC TGC CCT GCG CAG GAG GTG GCA AGA
Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg>

  100         110         120         130         140
    *   *   *   *   *   *   *   *   *   *   *   *   *
GGC GTG CTG ACC AGT CTG CCA GGA GAC AGC GTG ACT CTG ACC TGC CCG
Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro>

    150         160         170         180         190
*   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GGG GTA GAG CCG GAA GAC AAT GCC ACT GTT CAC TGG GTG CTC AGG AAG
Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys>

        200         210         220         230         240
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CCG GCT GCA GGC TCC CAC CCC AGC AGA TGG GCT GGC ATG GGA AGG AGG
Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg>

          250         260         270         280
      *   *   *   *   *   *   *   *   *   *   *   *   *
CTG CTG CTG AGG TCG GTG CAG CTC CAC GAC TCT GGA AAC TAT TCA TGC
Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys>

290         300         310         320         330
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
TAC CGG GCC GGC CGC CCA GCT GGG ACT GTG CAC TTG CTG GTG GAT GTT
Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val>

  340         350         360         370         380
    *   *   *   *   *   *   *   *   *   *   *   *   *
CCC CCC GAG GAG CCC CAG CTC TCC TGC TTC CGG AAG AGC CCC CTC AGC
Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser>

    390         400         410         420         430
*   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AAT GTT GTT TGT GAG TGG GGT CCT CGG AGC ACC CCA TCC CTG ACG ACA
Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr>

        440         450         460         470         480
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AAG GCT GTG CTC TTG GTG AGG AAG TTT CAG AAC AGT CCG GCC GAA GAC
Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp>

          490         500         510         520
      *   *   *   *   *   *   *   *   *   *   *   *   *
TTC CAG GAG CCG TGC CAG TAT TCC CAG GAG TCC CAG AAG TTC TCC TGC
Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys>

530         540         550         560         570
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CAG TTA GCA GTC CCG GAG GGA GAC AGC TCT TTC TAC ATA GTG TCC ATG
Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met>
```

Fig.25B.


```
  580          590          600          610          620
   *    *       *    *       *    *       *    *       *
TGC GTC GCC AGT AGT GTC GGG AGC AAG TTC AGC AAA ACT CAA ACC TTT
Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe>

    630          640          650          660          670
*    *       *    *       *    *       *    *       *    *
CAG GGT TGT GGA ATC TTG CAG CCT GAT CCG CCT GCC AAC ATC ACA GTC
Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val>

        680          690          700          710          720
  *    *       *    *       *    *       *    *       *    *
ACT GCC GTG GCC AGA AAC CCC CGC TGG CTC AGT GTC ACC TGG CAA GAC
Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp>

          730          740          750          760
     *    *       *    *       *    *       *    *       *
CCC CAC TCC TGG AAC TCA TCT TTC TAC AGA CTA CGG TTT GAG CTC AGA
Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg>

770          780          790          800          810
  *    *       *    *       *    *       *    *       *    *
TAT CGG GCT GAA CGG TCA AAG ACA TTC ACA ACA TGG ATG GTC AAG GAC
Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp>

  820          830          840          850          860
   *    *       *    *       *    *       *    *       *
CTC CAG CAT CAC TGT GTC ATC CAC GAC GCC TGG AGC GGC CTG AGG CAC
Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His>

    870          880          890          900          910
*    *       *    *       *    *       *    *       *    *
GTG GTG CAG CTT CGT GCC CAG GAG GAG TTC GGG CAA GGC GAG TGG AGC
Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser>

        920          930          940          950          960
  *    *       *    *       *    *       *    *       *    *
GAG TGG AGC CCG GAG GCC ATG GGC ACG CCT TGG ACA GAA TCG CGA TCG
Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser>

          970          980          990          1000
     *    *       *    *       *    *       *    *       *
CCT CCA GCT GAG AAC GAG GTG TCC ACC CCC ATG GAA CTT CTA GAC CCA
Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Glu Leu Leu Asp Pro>

1010         1020         1030         1040         1050
  *    *       *    *       *    *       *    *       *    *
TGT GGT TAT ATC AGT CCT GAA TCT CCA GTT GTA CAA CTT CAT TCT AAT
Cys Gly Tyr Ile Ser Pro Glu Ser Pro Val Val Gln Leu His Ser Asn>

  1060         1070         1080         1090         1100
   *    *       *    *       *    *       *    *       *
TTC ACT GCA GTT TGT GTG CTA AAG GAA AAA TGT ATG GAT TAT TTT CAT
Phe Thr Ala Val Cys Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His>

    1110         1120         1130         1140         1150
*    *       *    *       *    *       *    *       *    *
GTA AAT GCT AAT TAC ATT GTC TGG AAA ACA AAC CAT TTT ACT ATT CCT
Val Asn Ala Asn Tyr Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro>

        1160         1170         1180         1190         1200
  *    *       *    *       *    *       *    *       *    *
```

Fig.25C.


```
AAG GAG CAA TAT ACT ATC ATA AAC AGA ACA GCA TCC AGT GTC ACC TTT
Lys Glu Gln Tyr Thr Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe>

        1210        1220        1230        1240
     *     *     *     *     *     *     *     *     *
ACA GAT ATA GCT TCA TTA AAT ATT CAG CTC ACT TGC AAC ATT CTT ACA
Thr Asp Ile Ala Ser Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr>

1250        1260        1270        1280        1290
  *     *     *     *     *     *     *     *     *     *
TTC GGA CAG CTT GAA CAG AAT GTT TAT GGA ATC ACA ATA ATT TCA GGC
Phe Gly Gln Leu Glu Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly>

 1300        1310        1320        1330        1340
    *     *     *     *     *     *     *     *     *
TTG CCT CCA GAA AAA CCT AAA AAT TTG AGT TGC ATT GTG AAC GAG GGG
Leu Pro Pro Glu Lys Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly>

   1350        1360        1370        1380        1390
*     *     *     *     *     *     *     *     *     *
AAG AAA ATG AGG TGT GAG TGG GAT GGT GGA AGG GAA ACA CAC TTG GAG
Lys Lys Met Arg Cys Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu>

      1400        1410        1420        1430        1440
  *     *     *     *     *     *     *     *     *     *
ACA AAC TTC ACT TTA AAA TCT GAA TGG GCA ACA CAC AAG TTT GCT GAT
Thr Asn Phe Thr Leu Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp>

        1450        1460        1470        1480
     *     *     *     *     *     *     *     *     *
TGC AAA GCA AAA CGT GAC ACC CCC ACC TCA TGC ACT GTT GAT TAT TCT
Cys Lys Ala Lys Arg Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser>

1490        1500        1510        1520        1530
  *     *     *     *     *     *     *     *     *     *
ACT GTG TAT TTT GTC AAC ATT GAA GTC TGG GTA GAA GCA GAG AAT GCC
Thr Val Tyr Phe Val Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala>

 1540        1550        1560        1570        1580
    *     *     *     *     *     *     *     *     *
CTT GGG AAG GTT ACA TCA GAT CAT ATC AAT TTT GAT CCT GTA TAT AAA
Leu Gly Lys Val Thr Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys>

   1590        1600        1610        1620        1630
*     *     *     *     *     *     *     *     *     *
GTG AAG CCC AAT CCG CCA CAT AAT TTA TCA GTG ATC AAC TCA GAG GAA
Val Lys Pro Asn Pro Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu>

      1640        1650        1660        1670        1680
  *     *     *     *     *     *     *     *     *     *
CTG TCT AGT ATC TTA AAA TTG ACA TGG ACC AAC CCA AGT ATT AAG AGT
Leu Ser Ser Ile Leu Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser>

        1690        1700        1710        1720
     *     *     *     *     *     *     *     *     *
GTT ATA ATA CTA AAA TAT AAC ATT CAA TAT AGG ACC AAA GAT GCC TCA
Val Ile Ile Leu Lys Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser>

1730        1740        1750        1760        1770
  *     *     *     *     *     *     *     *     *     *
ACT TGG AGC CAG ATT CCT CCT GAA GAC ACA GCA TCC ACC CGA TCT TCA
Thr Trp Ser Gln Ile Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser>
```

Fig.25D.


```
1780          1790          1800          1810          1820
   *     *       *       *     *       *       *     *       *
TTC ACT GTC CAA GAC CTT AAA CCT TTT ACA GAA TAT GTG TTT AGG ATT
Phe Thr Val Gln Asp Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile>

   1830          1840          1850          1860          1870
*     *       *       *     *       *       *     *       *     *
CGC TGT ATG AAG GAA GAT GGT AAG GGA TAC TGG AGT GAC TGG AGT GAA
Arg Cys Met Lys Glu Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu>

      1880          1890          1900          1910          1920
  *     *       *     *       *       *     *       *     *     *
GAA GCA AGT GGG ATC ACC TAT GAA GAT AGA CCA TCT AAA GCA CCA AGT
Glu Ala Ser Gly Ile Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser>

         1930          1940          1950          1960
     *     *       *       *     *       *       *     *     *
TTC TGG TAT AAA ATA GAT CCA TCC CAT ACT CAA GGC TAC AGA ACT GTA
Phe Trp Tyr Lys Ile Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val>

1970          1980          1990          2000          2010
   *     *       *       *     *       *       *     *       *
CAA CTC GTG TGG AAG ACA TTG CCT CCT TTT GAA GCC AAT GGA AAA ATC
Gln Leu Val Trp Lys Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile>

   2020          2030          2040          2050          2060
      *     *       *       *     *       *       *     *       *
TTG GAT TAT GAA GTG ACT CTC ACA AGA TGG AAA TCA CAT TTA CAA AAT
Leu Asp Tyr Glu Val Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn>

   2070          2080          2090          2100          2110
*     *       *       *     *       *       *     *       *     *
TAC ACA GTT AAT GCC ACA AAA CTG ACA GTA AAT CTC ACA AAT GAT CGC
Tyr Thr Val Asn Ala Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg>

      2120          2130          2140          2150          2160
  *     *       *     *       *       *     *       *     *     *
TAT CTA GCA ACC CTA ACA GTA AGA AAT CTT GTT GGC AAA TCA GAT GCA
Tyr Leu Ala Thr Leu Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala>

         2170          2180          2190          2200
     *     *       *       *     *       *       *     *     *
GCT GTT TTA ACT ATC CCT GCC TGT GAC TTT CAA GCT ACT CAC CCT GTA
Ala Val Leu Thr Ile Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val>

2210          2220          2230          2240          2250
   *     *       *       *     *       *       *     *       *
ATG GAT CTT AAA GCA TTC CCC AAA GAT AAC ATG CTT TGG GTG GAA TGG
Met Asp Leu Lys Ala Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp>

   2260          2270          2280          2290          2300
      *     *       *       *     *       *       *     *       *
ACT ACT CCA AGG GAA TCT GTA AAG AAA TAT ATA CTT GAG TGG TGT GTG
Thr Thr Pro Arg Glu Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val>

   2310          2320          2330          2340          2350
*     *       *       *     *       *       *     *       *     *
TTA TCA GAT AAA GCA CCC TGT ATC ACA GAC TGG CAA CAA GAA GAT GGT
Leu Ser Asp Lys Ala Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly>

      2360          2370          2380          2390          2400
```

Fig.25E.


```
  *       *       *       *       *       *       *       *       *       *
ACC GTG CAT CGC ACC TAT TTA AGA GGG AAC TTA GCA GAG AGC AAA TGC
Thr Val His Arg Thr Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys>

          2410          2420          2430          2440
      *       *       *       *       *       *       *       *
TAT TTG ATA ACA GTT ACT CCA GTA TAT GCT GAT GGA CCA GGA AGC CCT
Tyr Leu Ile Thr Val Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro>

2450          2460          2470          2480          2490
  *       *       *       *       *       *       *       *       *
GAA TCC ATA AAG GCA TAC CTT AAA CAA GCT CCA CCT TCC AAA GGA CCT
Glu Ser Ile Lys Ala Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro>

 2500          2510          2520          2530          2540
    *       *       *       *       *       *       *       *
ACT GTT CGG ACA AAA AAA GTA GGG AAA AAC GAA GCT GTC TTA GAG TGG
Thr Val Arg Thr Lys Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp>

   2550          2560          2570          2580          2590
  *       *       *       *       *       *       *       *       *
GAC CAA CTT CCT GTT GAT GTT CAG AAT GGA TTT ATC AGA AAT TAT ACT
Asp Gln Leu Pro Val Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr>

       2600          2610          2620          2630          2640
   *       *       *       *       *       *       *       *       *
ATA TTT TAT AGA ACC ATC ATT GGA AAT GAA ACT GCT GTG AAT GTG GAT
Ile Phe Tyr Arg Thr Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp>

          2650          2660          2670          2680
      *       *       *       *       *       *       *       *       *
TCT TCC CAC ACA GAA TAT ACA TTG TCC TCT TTG ACT AGT GAC ACA TTG
Ser Ser His Thr Glu Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu>

2690          2700          2710          2720          2730
  *       *       *       *       *       *       *       *       *
TAC ATG GTA CGA ATG GCA GCA TAC ACA GAT GAA GGT GGG AAG GAT GGT
Tyr Met Val Arg Met Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly>

 2740          2750          2760          2770          2780
    *       *       *       *       *       *       *       *
CCA GAA TTC ACT TTT ACT ACC CCA AAG TTT GCT CAA GGA GAA ATT GAA
Pro Glu Phe Thr Phe Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu>

   2790          2800          2810          2820          2830
  *       *       *       *       *       *       *       *       *
TCC GGG GGC GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA
Ser Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu>

       2840          2850          2860          2870          2880
   *       *       *       *       *       *       *       *       *
CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp>

          2890          2900          2910          2920
      *       *       *       *       *       *       *       *       *
ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp>

2930          2940          2950          2960          2970
  *       *       *       *       *       *       *       *       *
GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC
```

Fig.25F.

```
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly>

 2980          2990          3000          3010          3020
    *     *       *     *     *     *       *     *       *
GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn>

   3030          3040          3050          3060          3070
*     *       *     *       *     *       *     *       *     *
AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp>

      3080          3090          3100          3110          3120
  *       *     *       *     *       *     *       *     *     *
CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro>

         3130          3140          3150          3160
      *     *       *     *       *     *       *     *     *
GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu>

3170          3180          3190          3200          3210
  *       *     *       *     *       *     *       *     *     *
CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn>

 3220          3230          3240          3250          3260
    *     *       *     *     *     *       *     *       *
CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile>

   3270          3280          3290          3300          3310
*     *       *     *       *     *       *     *       *     *
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr>

      3320          3330          3340          3350          3360
  *       *     *       *     *       *     *       *     *     *
ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys>

         3370          3380          3390          3400
      *     *       *     *       *     *       *     *     *
CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys>

3410          3420          3430          3440          3450
  *       *     *       *     *       *     *       *     *     *
TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu>

 3460          3470
    *     *       *     *
TCC CTG TCT CCG GGT AAA TGA
Ser Leu Ser Pro Gly Lys ***>
```

Fig.26A.


```
          10          20          30          40
      *   *   *   *   *   *   *   *   *   *
ATG GTG CTT CTG TGG TGT GTA GTG AGT CTC TAC TTT TAT GGA ATC CTG
Met Val Leu Leu Trp Cys Val Val Ser Leu Tyr Phe Tyr Gly Ile Leu>

50          60          70          80          90
 *   *   *   *   *   *   *   *   *   *   *   *
CAA AGT GAT GCC TCA GAA CGC TGC GAT GAC TGG GGA CTA GAC ACC ATG
Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met>

  100         110         120         130         140
    *   *   *   *   *   *   *   *   *   *   *   *
AGG CAA ATC CAA GTG TTT GAA GAT GAG CCA GCT CGC ATC AAG TGC CCA
Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro>

    150         160         170         180         190
*   *   *   *   *   *   *   *   *   *   *   *   *   *
CTC TTT GAA CAC TTC TTG AAA TTC AAC TAC AGC ACA GCC CAT TCA GCT
Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala>

      200         210         220         230         240
  *   *   *   *   *   *   *   *   *   *   *   *   *   *
GGC CTT ACT CTG ATC TGG TAT TGG ACT AGG CAG GAC CGG GAC CTT GAG
Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu>

          250         260         270         280
      *   *   *   *   *   *   *   *   *   *   *
GAG CCA ATT AAC TTC CGC CTC CCC GAG AAC CGC ATT AGT AAG GAG AAA
Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys>

290         300         310         320         330
  *   *   *   *   *   *   *   *   *   *   *   *
GAT GTG CTG TGG TTC CGG CCC ACT CTC CTC AAT GAC ACT GGC AAC TAT
Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr>

  340         350         360         370         380
    *   *   *   *   *   *   *   *   *   *   *   *
ACC TGC ATG TTA AGG AAC ACT ACA TAT TGC AGC AAA GTT GCA TTT CCC
Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro>

    390         400         410         420         430
*   *   *   *   *   *   *   *   *   *   *   *   *   *
TTG GAA GTT GTT CAA AAA GAC AGC TGT TTC AAT TCC CCC ATG AAA CTC
Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu>

      440         450         460         470         480
  *   *   *   *   *   *   *   *   *   *   *   *   *   *
CCA GTG CAT AAA CTG TAT ATA GAA TAT GGC ATT CAG AGG ATC ACT TGT
Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys>

          490         500         510         520
      *   *   *   *   *   *   *   *   *   *   *
CCA AAT GTA GAT GGA TAT TTT CCT TCC AGT GTC AAA CCG ACT ATC ACT
Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr>

530         540         550         560         570
  *   *   *   *   *   *   *   *   *   *   *   *
TGG TAT ATG GGC TGT TAT AAA ATA CAG AAT TTT AAT AAT GTA ATA CCC
Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro>
```

Fig.26B.


```
  580         590         600         610         620
    *     *     *     *     *     *     *     *     *
GAA GGT ATG AAC TTG AGT TTC CTC ATT GCC TTA ATT TCA AAT AAT GGA
Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly>

    630         640         650         660         670
*     *     *     *     *     *     *     *     *     *
AAT TAC ACA TGT GTT GTT ACA TAT CCA GAA AAT GGA CGT ACG TTT CAT
Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His>

      680         690         700         710         720
  *     *     *     *     *     *     *     *     *     *
CTC ACC AGG ACT CTG ACT GTA AAG GTA GTA GGC TCT CCA AAA AAT GCA
Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala>

          730         740         750         760
    *     *     *     *     *     *     *     *     *
GTG CCC CCT GTG ATC CAT TCA CCT AAT GAT CAT GTG GTC TAT GAG AAA
Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys>

770         780         790         800         810
  *     *     *     *     *     *     *     *     *     *
GAA CCA GGA GAG GAG CTA CTC ATT CCC TGT ACG GTC TAT TTT AGT TTT
Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe>

  820         830         840         850         860
    *     *     *     *     *     *     *     *     *
CTG ATG GAT TCT CGC AAT GAG GTT TGG TGG ACC ATT GAT GGA AAA AAA
Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys>

    870         880         890         900         910
*     *     *     *     *     *     *     *     *     *
CCT GAT GAC ATC ACT ATT GAT GTC ACC ATT AAC GAA AGT ATA AGT CAT
Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His>

      920         930         940         950         960
  *     *     *     *     *     *     *     *     *     *
AGT AGA ACA GAA GAT GAA ACA AGA ACT CAG ATT TTG AGC ATC AAG AAA
Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys>

          970         980         990         1000
    *     *     *     *     *     *     *     *     *
GTT ACC TCT GAG GAT CTC AAG CGC AGC TAT GTC TGT CAT GCT AGA AGT
Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser>

1010        1020        1030        1040        1050
  *     *     *     *     *     *     *     *     *     *
GCC AAA GGC GAA GTT GCC AAA GCA GCC AAG GTG AAG CAG AAA GTG CCA
Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro>

  1060        1070        1080        1090        1100
    *     *     *     *     *     *     *     *     *
GCT CCA AGA TAC ACA GTG TCC GGT GGC GCG CCT ATG CTG AGC GAG GCT
Ala Pro Arg Tyr Thr Val Ser Gly Gly Ala Pro Met Leu Ser Glu Ala>

    1110        1120        1130        1140        1150
*     *     *     *     *     *     *     *     *     *
GAT AAA TGC AAG GAA CGT GAA GAA AAA ATA ATT TTA GTG TCA TCT GCA
Asp Lys Cys Lys Glu Arg Glu Glu Lys Ile Ile Leu Val Ser Ser Ala>

      1160        1170        1180        1190        1200
  *     *     *     *     *     *     *     *     *     *
```

Fig.26C.


```
AAT GAA ATT GAT GTT CGT CCC TGT CCT CTT AAC CCA AAT GAA CAC AAA
Asn Glu Ile Asp Val Arg Pro Cys Pro Leu Asn Pro Asn Glu His Lys>

          1210         1220         1230         1240
      *    *    *    *    *    *    *    *    *    *
GGC ACT ATA ACT TGG TAT AAG GAT GAC AGC AAG ACA CCT GTA TCT ACA
Gly Thr Ile Thr Trp Tyr Lys Asp Asp Ser Lys Thr Pro Val Ser Thr>

1250         1260         1270         1280         1290
  *    *    *    *    *    *    *    *    *    *    *
GAA CAA GCC TCC AGG ATT CAT CAA CAC AAA GAG AAA CTT TGG TTT GTT
Glu Gln Ala Ser Arg Ile His Gln His Lys Glu Lys Leu Trp Phe Val>

 1300         1310         1320         1330         1340
    *    *    *    *    *    *    *    *    *    *
CCT GCT AAG GTG GAG GAT TCA GGA CAT TAC TAT TGC GTG GTA AGA AAT
Pro Ala Lys Val Glu Asp Ser Gly His Tyr Tyr Cys Val Val Arg Asn>

   1350         1360         1370         1380         1390
*    *    *    *    *    *    *    *    *    *    *    *
TCA TCT TAC TGC CTC AGA ATT AAA ATA AGT GCA AAA TTT GTG GAG AAT
Ser Ser Tyr Cys Leu Arg Ile Lys Ile Ser Ala Lys Phe Val Glu Asn>

      1400         1410         1420         1430         1440
  *    *    *    *    *    *    *    *    *    *    *    *
GAG CCT AAC TTA TGT TAT AAT GCA CAA GCC ATA TTT AAG CAG AAA CTA
Glu Pro Asn Leu Cys Tyr Asn Ala Gln Ala Ile Phe Lys Gln Lys Leu>

          1450         1460         1470         1480
      *    *    *    *    *    *    *    *    *    *
CCC GTT GCA GGA GAC GGA GGA CTT GTG TGC CCT TAT ATG GAG TTT TTT
Pro Val Ala Gly Asp Gly Gly Leu Val Cys Pro Tyr Met Glu Phe Phe>

1490         1500         1510         1520         1530
  *    *    *    *    *    *    *    *    *    *    *
AAA AAT GAA AAT AAT GAG TTA CCT AAA TTA CAG TGG TAT AAG GAT TGC
Lys Asn Glu Asn Asn Glu Leu Pro Lys Leu Gln Trp Tyr Lys Asp Cys>

 1540         1550         1560         1570         1580
    *    *    *    *    *    *    *    *    *    *
AAA CCT CTA CTT CTT GAC AAT ATA CAC TTT AGT GGA GTC AAA GAT AGG
Lys Pro Leu Leu Leu Asp Asn Ile His Phe Ser Gly Val Lys Asp Arg>

   1590         1600         1610         1620         1630
*    *    *    *    *    *    *    *    *    *    *    *
CTC ATC GTG ATG AAT GTG GCT GAA AAG CAT AGA GGG AAC TAT ACT TGT
Leu Ile Val Met Asn Val Ala Glu Lys His Arg Gly Asn Tyr Thr Cys>

      1640         1650         1660         1670         1680
  *    *    *    *    *    *    *    *    *    *    *    *
CAT GCA TCC TAC ACA TAC TTG GGC AAG CAA TAT CCT ATT ACC CGG GTA
His Ala Ser Tyr Thr Tyr Leu Gly Lys Gln Tyr Pro Ile Thr Arg Val>

          1690         1700         1710         1720
      *    *    *    *    *    *    *    *    *    *
ATA GAA TTT ATT ACT CTA GAG GAA AAC AAA CCC ACA AGG CCT GTG ATT
Ile Glu Phe Ile Thr Leu Glu Glu Asn Lys Pro Thr Arg Pro Val Ile>

1730         1740         1750         1760         1770
  *    *    *    *    *    *    *    *    *    *    *
GTG AGC CCA GCT AAT GAG ACA ATG GAA GTA GAC TTG GGA TCC CAG ATA
Val Ser Pro Ala Asn Glu Thr Met Glu Val Asp Leu Gly Ser Gln Ile>
```

Fig.26D.


```
 1780          1790          1800          1810          1820
    *     *       *     *       *     *       *     *       *
CAA TTG ATC TGT AAT GTC ACC GGC CAG TTG AGT GAC ATT GCT TAC TGG
Gln Leu Ile Cys Asn Val Thr Gly Gln Leu Ser Asp Ile Ala Tyr Trp>

   1830          1840          1850          1860          1870
*     *       *     *       *     *       *     *       *     *
AAG TGG AAT GGG TCA GTA ATT GAT GAA GAT GAC CCA GTG CTA GGG GAA
Lys Trp Asn Gly Ser Val Ile Asp Glu Asp Asp Pro Val Leu Gly Glu>

      1880          1890          1900          1910          1920
  *     *       *     *       *     *       *     *       *     *
GAC TAT TAC AGT GTG GAA AAT CCT GCA AAC AAA AGA AGG AGT ACC CTC
Asp Tyr Tyr Ser Val Glu Asn Pro Ala Asn Lys Arg Arg Ser Thr Leu>

         1930          1940          1950          1960
     *     *       *     *       *     *       *     *
ATC ACA GTG CTT AAT ATA TCG GAA ATT GAG AGT AGA TTT TAT AAA CAT
Ile Thr Val Leu Asn Ile Ser Glu Ile Glu Ser Arg Phe Tyr Lys His>

1970          1980          1990          2000          2010
  *     *       *     *       *     *       *     *       *
CCA TTT ACC TGT TTT GCC AAG AAT ACA CAT GGT ATA GAT GCA GCA TAT
Pro Phe Thr Cys Phe Ala Lys Asn Thr His Gly Ile Asp Ala Ala Tyr>

 2020          2030          2040          2050          2060
    *     *       *     *       *     *       *     *       *
ATC CAG TTA ATA TAT CCA GTC ACT AAT TCC GGA GAC AAA ACT CAC ACA
Ile Gln Leu Ile Tyr Pro Val Thr Asn Ser Gly Asp Lys Thr His Thr>

   2070          2080          2090          2100          2110
*     *       *     *       *     *       *     *       *     *
TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe>

      2120          2130          2140          2150          2160
  *     *       *     *       *     *       *     *       *     *
CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro>

         2170          2180          2190          2200
     *     *       *     *       *     *       *     *
GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val>

2210          2220          2230          2240          2250
  *     *       *     *       *     *       *     *       *
AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr>

 2260          2270          2280          2290          2300
    *     *       *     *       *     *       *     *       *
AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val>

   2310          2320          2330          2340          2350
*     *       *     *       *     *       *     *       *     *
CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys>

      2360          2370          2380          2390          2400
```

Fig.26E.

```
   *       *       *       *       *       *       *       *       *       *
AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser>

          2410          2420          2430          2440
       *       *       *       *       *       *       *       *
AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro>

2450          2460          2470          2480          2490
   *       *       *       *       *       *       *       *       *
TCC CGG GAG GAG ATG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC
Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val>

 2500          2510          2520          2530          2540
    *       *       *       *       *       *       *       *
AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly>

   2550          2560          2570          2580          2590
*       *       *       *       *       *       *       *       *
CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp>

       2600          2610          2620          2630          2640
   *       *       *       *       *       *       *       *       *
GGC TCC TTC TTC CTC TAT AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp>

          2650          2660          2670          2680
       *       *       *       *       *       *       *       *
CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His>

2690          2700          2710          2720          2730
   *       *       *       *       *       *       *       *
AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys ***>
```

Fig.27.

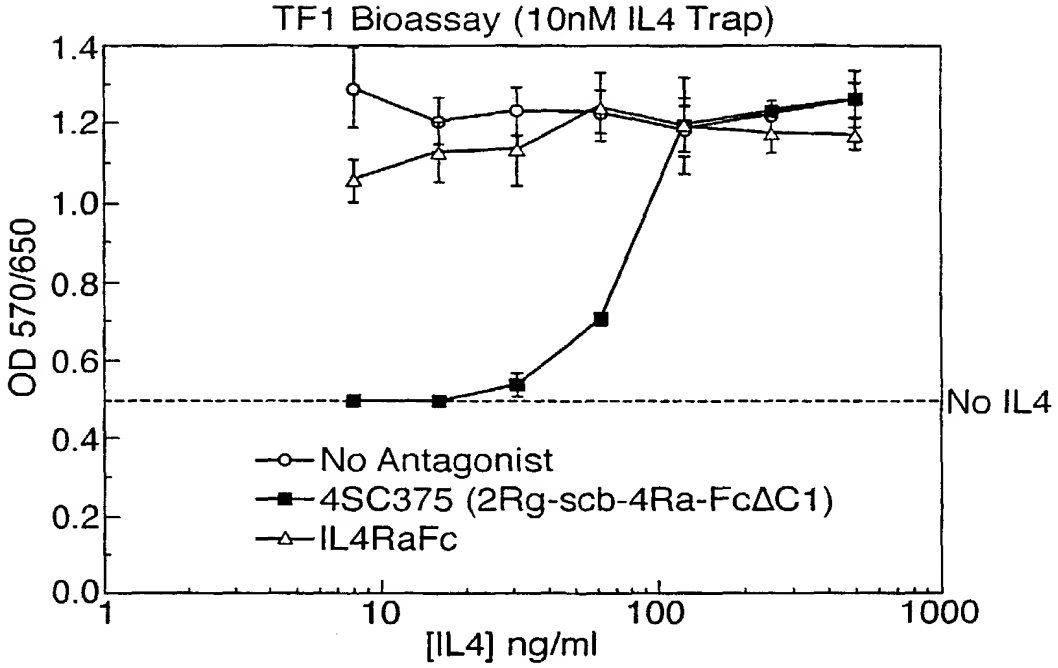

TF1 Bioassay (10nM IL4 Trap)
OD 570/650
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
No IL4
No Antagonist
4SC375 (2Rg-scb-4Ra-FcΔC1)
IL4RaFc
1
10
100
1000
[IL4] ng/ml

Fig.28.

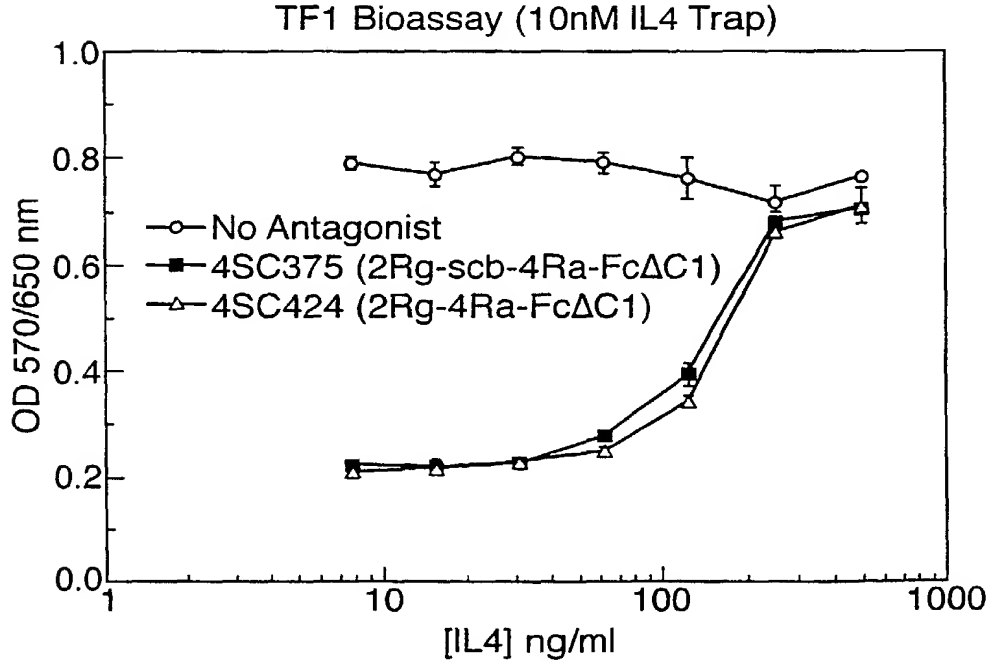

TF1 Bioassay (10nM IL4 Trap)
OD 570/650 nm
1.0
0.8
0.6
0.4
0.2
0.0
No Antagonist
4SC375 (2Rg-scb-4Ra-FcΔC1)
4SC424 (2Rg-4Ra-FcΔC1)
1
10
100
1000
[IL4] ng/ml

Fig.29.

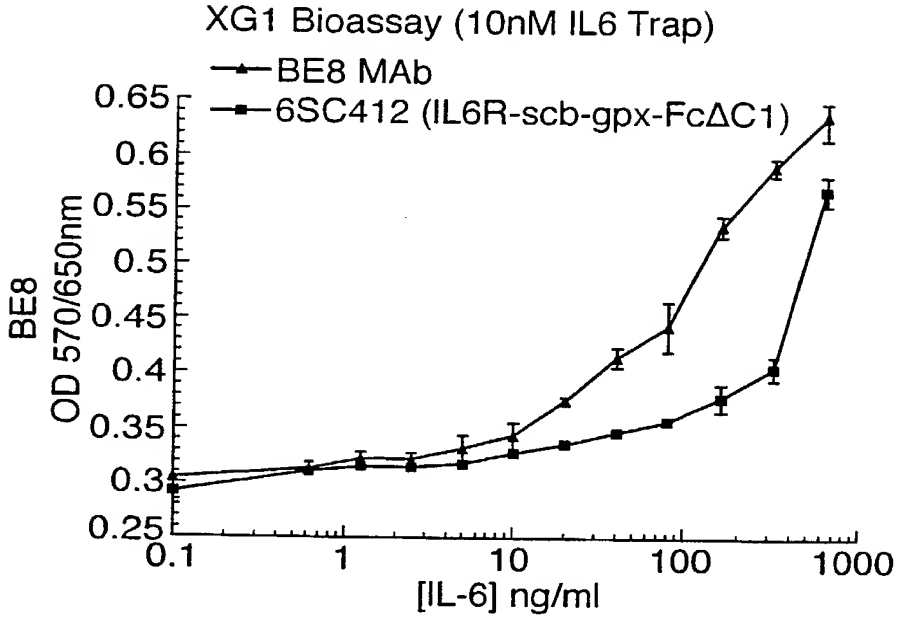

XG1 Bioassay (10nM IL6 Trap)
BE8 MAb
6SC412 (IL6R-scb-gpx-FcΔC1)
BE8
OD 570/650nm
0.65
0.6
0.55
0.5
0.45
0.4
0.35
0.3
0.25
0.1
1
10
100
1000
[IL-6] ng/ml

Fig.30.

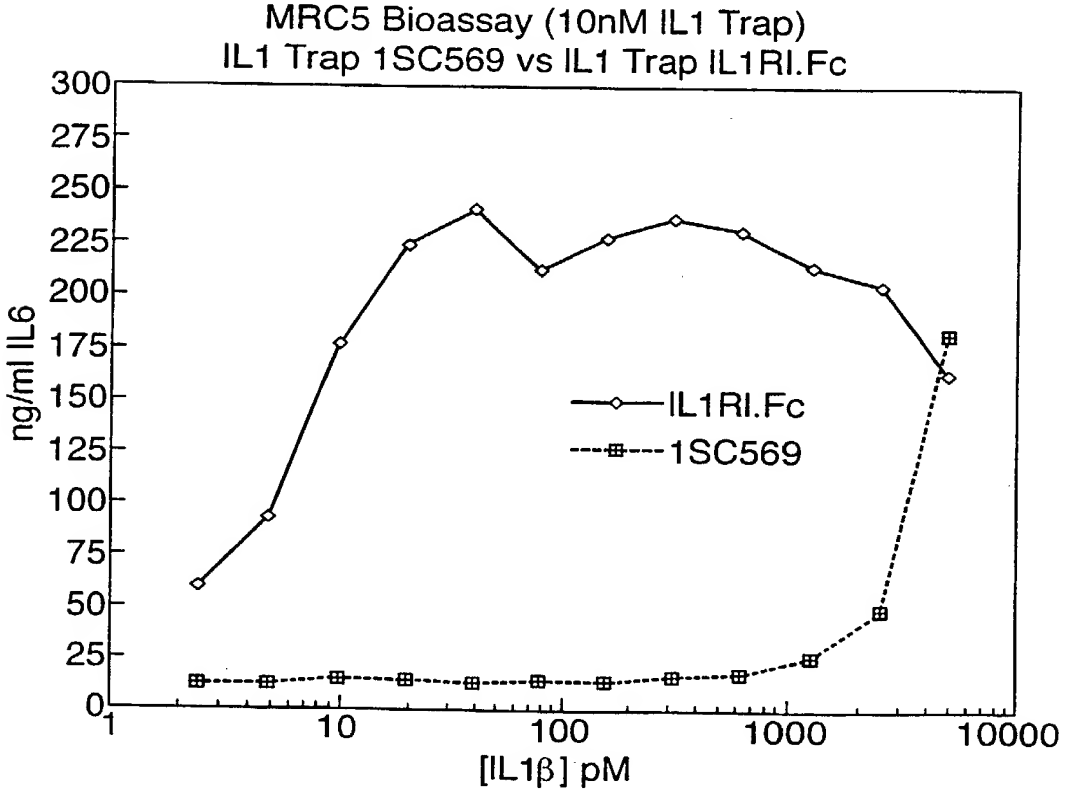

MRC5 Bioassay (10nM IL1 Trap)
IL1 Trap 1SC569 vs IL1 Trap IL1RI.Fc
ng/ml IL6
300
275
250
225
200
175
150
125
100
75
50
25
0
1
10
100
1000
10000
[IL1β] pM
IL1RI.Fc
1SC569

Fig.31A.

```
          10          20          30          40
     *    *    *     *    *     *    *     *    *
ATG GTG TGG CTT TGC TCT GGG CTC CTG TTC CCT GTG AGC TGC CTG GTC
TAC CAC ACC GAA ACG AGA CCC GAG GAC AAG GGA CAC TCG ACG GAC CAG
Met Val Trp Leu Cys Ser Gly Leu Leu Phe Pro Val Ser Cys Leu Val>

50          60          70          80          90
 *     *     *     *     *     *     *     *     *     *
CTG CTG CAG GTG GCA AGC TCT GGG AAC ATG AAG GTC TTG CAG GAG CCC
GAC GAC GTC CAC CGT TCG AGA CCC TTG TAC TTC CAG AAC GTC CTC GGG
Leu Leu Gln Val Ala Ser Ser Gly Asn Met Lys Val Leu Gln Glu Pro>

  100         110         120         130         140
    *     *     *     *     *     *     *     *     *
ACC TGC GTC TCC GAC TAC ATG AGC ATC TCT ACT TGC GAG TGG AAG ATG
TGG ACG CAG AGG CTG ATG TAC TCG TAG AGA TGA ACG CTC ACC TTC TAC
Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met>

    150         160         170         180         190
*     *     *     *     *     *     *     *     *     *
AAT GGT CCC ACC AAT TGC AGC ACC GAG CTC CGC CTG TTG TAC CAG CTG
TTA CCA GGG TGG TTA ACG TCG TGG CTC GAG GCG GAC AAC ATG GTC GAC
Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu>

       200         210         220         230         240
  *     *     *     *     *     *     *     *     *     *
GTT TTT CTG CTC TCC GAA GCC CAC ACG TGT ATC CCT GAG AAC AAC GGA
CAA AAA GAC GAG AGG CTT CGG GTG TGC ACA TAG GGA CTC TTG TTG CCT
Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly>

          250         260         270         280
     *    *     *     *     *     *     *     *     *
GGC GCG GGG TGC GTG TGC CAC CTG CTC ATG GAT GAC GTG GTC AGT GCG
CCG CGC CCC ACG CAC ACG GTG GAC GAG TAC CTA CTG CAC CAG TCA CGC
Gly Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala>

290         300         310         320         330
 *     *     *     *     *     *     *     *     *     *
GAT AAC TAT ACA CTG GAC CTG TGG GCT GGG CAG CAG CTG CTG TGG AAG
CTA TTG ATA TGT GAC CTG GAC ACC CGA CCC GTC GTC GAC GAC ACC TTC
Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys>

  340         350         360         370         380
    *     *     *     *     *     *     *     *     *
GGC TCC TTC AAG CCC AGC GAG CAT GTG AAA CCC AGG GCC CCA GGA AAC
CCG AGG AAG TTC GGG TCG CTC GTA CAC TTT GGG TCC CGG GGT CCT TTG
Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn>
```

Fig.31B.

```
     390           400           410           420           430
 *     *     *     *     *     *     *     *     *     *     *
CTG ACA GTT CAC ACC AAT GTC TCC GAC ACT CTG CTG CTG ACC TGG AGC
GAC TGT CAA GTG TGG TTA CAG AGG CTG TGA GAC GAC GAC TGG ACC TCG
Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser>

        440           450           460           470           480
   *     *     *     *     *     *     *     *     *     *     *
AAC CCG TAT CCC CCT GAC AAT TAC CTG TAT AAT CAT CTC ACC TAT GCA
TTG GGC ATA GGG GGA CTG TTA ATG GAC ATA TTA GTA GAG TGG ATA CGT
Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala>

          490           500           510           520
      *     *     *     *     *     *     *     *     *
GTC AAC ATT TGG AGT GAA AAC GAC CCG GCA GAT TTC AGA ATC TAT AAC
CAG TTG TAA ACC TCA CTT TTG CTG GGC CGT CTA AAG TCT TAG ATA TTG
Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn>

530           540           550           560           570
  *     *     *     *     *     *     *     *     *     *     *
GTG ACC TAC CTA GAA CCC TCC CTC CGC ATC GCA GCC AGC ACC CTG AAG
CAC TGG ATG GAT CTT GGG AGG GAG GCG TAG CGT CGG TCG TGG GAC TTC
Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys>

   580           590           600           610           620
     *     *     *     *     *     *     *     *     *     *
TCT GGG ATT TCC TAC AGG GCA CGG GTG AGG GCC TGG GCT CAG AGC TAT
AGA CCC TAA AGG ATG TCC CGT GCC CAC TCC CGG ACC CGA GTC TCG ATA
Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Ser Tyr>

     630           640           650           660           670
 *     *     *     *     *     *     *     *     *     *     *
AAC ACC ACC TGG AGT GAG TGG AGC CCC AGC ACC AAG TGG CAC AAC TCC
TTG TGG TGG ACC TCA CTC ACC TCG GGG TCG TGG TTC ACC GTG TTG AGG
Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser>

        680           690           700           710           720
   *     *     *     *     *     *     *     *     *     *     *
TAC AGG GAG CCC TTC GAG CAG TCC GGT GGG GGC GGG GGC GCC GCG CCT
ATG TCC CTC GGG AAG CTC GTC AGG CCA CCC CCG CCC CCG CGG CGC GGA
Tyr Arg Glu Pro Phe Glu Gln Ser Gly Gly Gly Gly Gly Ala Ala Pro>

          730           740           750           760
      *     *     *     *     *     *     *     *     *
ACG GAA ACT CAG CCA CCT GTG ACA AAT TTG AGT GTC TCT GTT GAA AAC
TGC CTT TGA GTC GGT GGA CAC TGT TTA AAC TCA CAG AGA CAA CTT TTG
Thr Glu Thr Gln Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn>
```

Fig.31C.

```
770          780          790          800          810
 *       *    *       *    *       *    *       *    *       *
CTC TGC ACA GTA ATA TGG ACA TGG AAT CCA CCC GAG GGA GCC AGC TCA
GAG ACG TGT CAT TAT ACC TGT ACC TTA GGT GGG CTC CCT CGG TCG AGT
Leu Cys Thr Val Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser>

  820          830          840          850          860
    *       *    *       *    *       *    *       *    *
AAT TGT AGT CTA TGG TAT TTT AGT CAT TTT GGC GAC AAA CAA GAT AAG
TTA ACA TCA GAT ACC ATA AAA TCA GTA AAA CCG CTG TTT GTT CTA TTC
Asn Cys Ser Leu Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys>

    870          880          890          900          910
*       *    *       *    *       *    *       *    *       *
AAA ATA GCT CCG GAA ACT CGT CGT TCA ATA GAA GTA CCC CTG AAT GAG
TTT TAT CGA GGC CTT TGA GCA GCA AGT TAT CTT CAT GGG GAC TTA CTC
Lys Ile Ala Pro Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu>

       920          930          940          950          960
  *       *    *       *    *       *    *       *    *       *
AGG ATT TGT CTG CAA GTG GGG TCC CAG TGT AGC ACC AAT GAG AGT GAG
TCC TAA ACA GAC GTT CAC CCC AGG GTC ACA TCG TGG TTA CTC TCA CTC
Arg Ile Cys Leu Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu>

          970          980          990          1000
     *       *    *       *    *       *    *       *    *
AAG CCT AGC ATT TTG GTT GAA AAA TGC ATC TCA CCC CCA GAA GGT GAT
TTC GGA TCG TAA AAC CAA CTT TTT ACG TAG AGT GGG GGT CTT CCA CTA
Lys Pro Ser Ile Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp>

1010         1020         1030         1040         1050
  *       *    *       *    *       *    *       *    *       *
CCT GAG TCT GCT GTG ACT GAG CTT CAA TGC ATT TGG CAC AAC CTG AGC
GGA CTC AGA CGA CAC TGA CTC GAA GTT ACG TAA ACC GTG TTG GAC TCG
Pro Glu Ser Ala Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser>

 1060         1070         1080         1090         1100
    *       *    *       *    *       *    *       *    *
TAC ATG AAG TGT TCT TGG CTC CCT GGA AGG AAT ACC AGT CCC GAC ACT
ATG TAC TTC ACA AGA ACC GAG GGA CCT TCC TTA TGG TCA GGG CTG TGA
Tyr Met Lys Cys Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr>

   1110         1120         1130         1140         1150
*       *    *       *    *       *    *       *    *       *
AAC TAT ACT CTC TAC TAT TGG CAC AGA AGC CTG GAA AAA ATT CAT CAA
TTG ATA TGA GAG ATG ATA ACC GTG TCT TCG GAC CTT TTT TAA GTA GTT
Asn Tyr Thr Leu Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln>
```

Fig.31D.

```
      1160         1170         1180         1190         1200
  *      *     *      *      *      *     *      *      *     *
TGT GAA AAC ATC TTT AGA GAA GGC CAA TAC TTT GGT TGT TCC TTT GAT
ACA CTT TTG TAG AAA TCT CTT CCG GTT ATG AAA CCA ACA AGG AAA CTA
Cys Glu Asn Ile Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp>

         1210         1220         1230         1240
     *      *     *      *      *     *      *      *     *
CTG ACC AAA GTG AAG GAT TCC AGT TTT GAA CAA CAC AGT GTC CAA ATA
GAC TGG TTT CAC TTC CTA AGG TCA AAA CTT GTT GTG TCA CAG GTT TAT
Leu Thr Lys Val Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile>

1250         1260         1270         1280         1290
  *      *     *      *      *      *     *      *      *
ATG GTC AAG GAT AAT GCA GGA AAA ATT AAA CCA TCC TTC AAT ATA GTG
TAC CAG TTC CTA TTA CGT CCT TTT TAA TTT GGT AGG AAG TTA TAT CAC
Met Val Lys Asp Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val>

 1300         1310         1320         1330         1340
    *     *      *      *      *     *      *     *      *
CCT TTA ACT TCC CGT GTG AAA CCT GAT CCT CCA CAT ATT AAA AAC CTC
GGA AAT TGA AGG GCA CAC TTT GGA CTA GGA GGT GTA TAA TTT TTG GAG
Pro Leu Thr Ser Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu>

   1350         1360         1370         1380         1390
 *     *      *      *      *      *     *      *      *     *
TCC TTC CAC AAT GAT GAC CTA TAT GTG CAA TGG GAG AAT CCA CAG AAT
AGG AAG GTG TTA CTA CTG GAT ATA CAC GTT ACC CTC TTA GGT GTC TTA
Ser Phe His Asn Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn>

      1400         1410         1420         1430         1440
  *      *     *      *      *      *     *      *      *     *
TTT ATT AGC AGA TGC CTA TTT TAT GAA GTA GAA GTC AAT AAC AGC CAA
AAA TAA TCG TCT ACG GAT AAA ATA CTT CAT CTT CAG TTA TTG TCG GTT
Phe Ile Ser Arg Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln>

         1450         1460         1470         1480
     *      *     *      *      *     *      *      *     *
ACT GAG ACA CAT AAT GTT TTC TAC GTC CAA GAG GCT AAA TGT GAG AAT
TGA CTC TGT GTA TTA CAA AAG ATG CAG GTT CTC CGA TTT ACA CTC TTA
Thr Glu Thr His Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn>

1490         1500         1510         1520         1530
  *      *     *      *      *      *     *      *      *
CCA GAA TTT GAG AGA AAT GTG GAG AAT ACA TCT TGT TTC ATG GTC CCT
GGT CTT AAA CTC TCT TTA CAC CTC TTA TGT AGA ACA AAG TAC CAG GGA
Pro Glu Phe Glu Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro>
```

Fig.31E.

```
 1540          1550          1560          1570          1580
    *     *       *     *     *     *       *     *       *
GGT GTT CTT CCT GAT ACT TTG AAC ACA GTC AGA ATA AGA GTC AAA ACA
CCA CAA GAA GGA CTA TGA AAC TTG TGT CAG TCT TAT TCT CAG TTT TGT
Gly Val Leu Pro Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr>

   1590          1600          1610          1620          1630
*     *       *     *     *     *       *     *       *     *
AAT AAG TTA TGC TAT GAG GAT GAC AAA CTC TGG AGT AAT TGG AGC CAA
TTA TTC AAT ACG ATA CTC CTA CTG TTT GAG ACC TCA TTA ACC TCG GTT
Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln>

      1640          1650          1660          1670          1680
  *       *     *       *     *       *     *       *     *     *
GAA ATG AGT ATA GGT AAG AAG CGC AAT TCC ACA ACC GGA GAC AAA ACT
CTT TAC TCA TAT CCA TTC TTC GCG TTA AGG TGT TGG CCT CTG TTT TGA
Glu Met Ser Ile Gly Lys Lys Arg Asn Ser Thr Thr Gly Asp Lys Thr>

         1690          1700          1710          1720
      *       *     *       *     *       *     *       *     *
CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA
GTG TGT ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser>

1730          1740          1750          1760          1770
   *       *     *       *     *       *     *       *     *
GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG
CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg>

 1780          1790          1800          1810          1820
    *     *       *     *     *     *       *     *       *
ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT
TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG CAC TCG GTG CTT CTG GGA
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro>

   1830          1840          1850          1860          1870
*     *       *     *     *     *       *     *       *     *
GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC
CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTA TTA CGG
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala>

      1880          1890          1900          1910          1920
  *       *     *       *     *       *     *       *     *     *
AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC
TTC TGT TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG GCA CAC CAG
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val>
```

Fig.31F.

```
          1930          1940          1950          1960
      *     *     *     *     *     *     *     *     *
AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC
TCG CAG GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr>

1970          1980          1990          2000          2010
  *     *     *     *     *     *     *     *     *     *
AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC
TTC ACG TTC CAG AGG TTG TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr>

  2020          2030          2040          2050          2060
    *     *     *     *     *     *     *     *     *     *
ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG
TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG GAC
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu>

    2070          2080          2090          2100          2110
*     *     *     *     *     *     *     *     *     *     *
CCC CCA TCC CGG GAG GAG ATG ACC AAG AAC CAG GTC AGC CTG ACC TGC
GGG GGT AGG GCC CTC CTC TAC TGG TTC TTG GTC CAG TCG GAC TGG ACG
Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys>

      2120          2130          2140          2150          2160
  *     *     *     *     *     *     *     *     *     *     *
CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC
GAC CAG TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC ACC CTC TCG
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser>

          2170          2180          2190          2200
      *     *     *     *     *     *     *     *     *
AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC
TTA CCC GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp>

2210          2220          2230          2240          2250
  *     *     *     *     *     *     *     *     *     *
TCC GAC GGC TCC TTC TTC CTC TAT AGC AAG CTC ACC GTG GAC AAG AGC
AGG CTG CCG AGG AAG AAG GAG ATA TCG TTC GAG TGG CAC CTG TTC TCG
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser>

  2260          2270          2280          2290          2300
    *     *     *     *     *     *     *     *     *     *
AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT
TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG AGG CAC TAC GTA CTC CGA
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala>
```

Fig.31G.

```
   2310          2320          2330          2340          2350
*     *       *     *     *     *     *     *     *       *
CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA
GAC GTG TTG GTG ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC CCA TTT
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys>

  *
TGA
ACT
***>
```

Fig.32A.

```
          10          20          30          40
     *    *    *    *    *    *    *    *    *
ATG GTG TGG CCG GCG CGG CTC TGC GGG CTG TGG GCG CTG CTG CTC TGC
TAC CAC ACC GGC CGC GCC GAG ACG CCC GAC ACC CGC GAC GAC GAG ACG
Met Val Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys>

50          60          70          80          90
 *    *    *    *    *    *    *    *    *    *
GCC GGC GGC GGG GGC GGG GGC GGG GGC GCC GCG CCT ACG GAA ACT CAG
CGG CCG CCG CCC CCG CCC CCG CCC CCG CGG CGC GGA TGC CTT TGA GTC
Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln>

  100         110         120         130         140
    *    *    *    *    *    *    *    *    *
CCA CCT GTG ACA AAT TTG AGT GTC TCT GTT GAA AAC CTC TGC ACA GTA
GGT GGA CAC TGT TTA AAC TCA CAG AGA CAA CTT TTG GAG ACG TGT CAT
Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val>

    150         160         170         180         190
*    *    *    *    *    *    *    *    *    *
ATA TGG ACA TGG AAT CCA CCC GAG GGA GCC AGC TCA AAT TGT AGT CTA
TAT ACC TGT ACC TTA GGT GGG CTC CCT CGG TCG AGT TTA ACA TCA GAT
Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu>

       200         210         220         230         240
  *    *    *    *    *    *    *    *    *    *
TGG TAT TTT AGT CAT TTT GGC GAC AAA CAA GAT AAG AAA ATA GCT CCG
ACC ATA AAA TCA GTA AAA CCG CTG TTT GTT CTA TTC TTT TAT CGA GGC
Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro>

          250         260         270         280
     *    *    *    *    *    *    *    *    *
GAA ACT CGT CGT TCA ATA GAA GTA CCC CTG AAT GAG AGG ATT TGT CTG
CTT TGA GCA GCA AGT TAT CTT CAT GGG GAC TTA CTC TCC TAA ACA GAC
Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu>

290         300         310         320         330
 *    *    *    *    *    *    *    *    *    *
CAA GTG GGG TCC CAG TGT AGC ACC AAT GAG AGT GAG AAG CCT AGC ATT
GTT CAC CCC AGG GTC ACA TCG TGG TTA CTC TCA CTC TTC GGA TCG TAA
Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile>

  340         350         360         370         380
    *    *    *    *    *    *    *    *    *
TTG GTT GAA AAA TGC ATC TCA CCC CCA GAA GGT GAT CCT GAG TCT GCT
AAC CAA CTT TTT ACG TAG AGT GGG GGT CTT CCA CTA GGA CTC AGA CGA
Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala>
```

Fig.32B.

```
    390           400           410           420           430
*     *     *     *     *     *     *     *     *     *
GTG ACT GAG CTT CAA TGC ATT TGG CAC AAC CTG AGC TAC ATG AAG TGT
CAC TGA CTC GAA GTT ACG TAA ACC GTG TTG GAC TCG ATG TAC TTC ACA
Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys>

       440           450           460           470           480
  *     *     *     *     *     *     *     *     *     *
TCT TGG CTC CCT GGA AGG AAT ACC AGT CCC GAC ACT AAC TAT ACT CTC
AGA ACC GAG GGA CCT TCC TTA TGG TCA GGG CTG TGA TTG ATA TGA GAG
Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu>

          490           500           510           520
     *     *     *     *     *     *     *     *     *
TAC TAT TGG CAC AGA AGC CTG GAA AAA ATT CAT CAA TGT GAA AAC ATC
ATG ATA ACC GTG TCT TCG GAC CTT TTT TAA GTA GTT ACA CTT TTG TAG
Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile>

530           540           550           560           570
  *     *     *     *     *     *     *     *     *     *
TTT AGA GAA GGC CAA TAC TTT GGT TGT TCC TTT GAT CTG ACC AAA GTG
AAA TCT CTT CCG GTT ATG AAA CCA ACA AGG AAA CTA GAC TGG TTT CAC
Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val>

  580           590           600           610           620
     *     *     *     *     *     *     *     *     *
AAG GAT TCC AGT TTT GAA CAA CAC AGT GTC CAA ATA ATG GTC AAG GAT
TTC CTA AGG TCA AAA CTT GTT GTG TCA CAG GTT TAT TAC CAG TTC CTA
Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp>

    630           640           650           660           670
*     *     *     *     *     *     *     *     *     *
AAT GCA GGA AAA ATT AAA CCA TCC TTC AAT ATA GTG CCT TTA ACT TCC
TTA CGT CCT TTT TAA TTT GGT AGG AAG TTA TAT CAC GGA AAT TGA AGG
Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser>

       680           690           700           710           720
  *     *     *     *     *     *     *     *     *     *
CGT GTG AAA CCT GAT CCT CCA CAT ATT AAA AAC CTC TCC TTC CAC AAT
GCA CAC TTT GGA CTA GGA GGT GTA TAA TTT TTG GAG AGG AAG GTG TTA
Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn>

          730           740           750           760
     *     *     *     *     *     *     *     *     *
GAT GAC CTA TAT GTG CAA TGG GAG AAT CCA CAG AAT TTT ATT AGC AGA
CTA CTG GAT ATA CAC GTT ACC CTC TTA GGT GTC TTA AAA TAA TCG TCT
Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg>
```

Fig.32C.

```
770          780          790          800          810
 *      *     *      *     *      *     *      *     *      *
TGC CTA TTT TAT GAA GTA GAA GTC AAT AAC AGC CAA ACT GAG ACA CAT
ACG GAT AAA ATA CTT CAT CTT CAG TTA TTG TCG GTT TGA CTC TGT GTA
Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His>

  820          830          840          850          860
    *     *      *     *      *     *      *     *      *
AAT GTT TTC TAC GTC CAA GAG GCT AAA TGT GAG AAT CCA GAA TTT GAG
TTA CAA AAG ATG CAG GTT CTC CGA TTT ACA CTC TTA GGT CTT AAA CTC
Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu>

    870          880          890          900          910
*     *      *     *      *     *      *     *      *     *
AGA AAT GTG GAG AAT ACA TCT TGT TTC ATG GTC CCT GGT GTT CTT CCT
TCT TTA CAC CTC TTA TGT AGA ACA AAG TAC CAG GGA CCA CAA GAA GGA
Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro>

       920          930          940          950          960
  *      *     *      *     *      *     *      *     *      *
GAT ACT TTG AAC ACA GTC AGA ATA AGA GTC AAA ACA AAT AAG TTA TGC
CTA TGA AAC TTG TGT CAG TCT TAT TCT CAG TTT TGT TTA TTC AAT ACG
Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys>

         970          980          990          1000
     *      *     *      *     *      *     *      *     *
TAT GAG GAT GAC AAA CTC TGG AGT AAT TGG AGC CAA GAA ATG AGT ATA
ATA CTC CTA CTG TTT GAG ACC TCA TTA ACC TCG GTT CTT TAC TCA TAT
Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile>

1010         1020         1030         1040         1050
  *      *     *      *     *      *     *      *     *      *
GGT AAG AAG CGC AAT TCC ACA GGC GCG CCT AGT GGT GGA GGT GGC CGG
CCA TTC TTC GCG TTA AGG TGT CCG CGC GGA TCA CCA CCT CCA CCG GCC
Gly Lys Lys Arg Asn Ser Thr Gly Ala Pro Ser Gly Gly Gly Gly Arg>

 1060         1070         1080         1090         1100
    *     *      *     *      *     *      *     *      *
CCC GCA AGC TCT GGG AAC ATG AAG GTC TTG CAG GAG CCC ACC TGC GTC
GGG CGT TCG AGA CCC TTG TAC TTC CAG AAC GTC CTC GGG TGG ACG CAG
Pro Ala Ser Ser Gly Asn Met Lys Val Leu Gln Glu Pro Thr Cys Val>

   1110         1120         1130         1140         1150
*     *      *     *      *     *      *     *      *     *
TCC GAC TAC ATG AGC ATC TCT ACT TGC GAG TGG AAG ATG AAT GGT CCC
AGG CTG ATG TAC TCG TAG AGA TGA ACG CTC ACC TTC TAC TTA CCA GGG
Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met Asn Gly Pro>
```

Fig.32D.

```
        1160          1170          1180          1190          1200
    *     *       *     *       *     *       *     *       *     *
ACC AAT TGC AGC ACC GAG CTC CGC CTG TTG TAC CAG CTG GTT TTT CTG
TGG TTA ACG TCG TGG CTC GAG GCG GAC AAC ATG GTC GAC CAA AAA GAC
Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu>

          1210          1220          1230          1240
      *     *       *     *       *     *       *     *     *
CTC TCC GAA GCC CAC ACG TGT ATC CCT GAG AAC AAC GGA GGC GCG GGG
GAG AGG CTT CGG GTG TGC ACA TAG GGA CTC TTG TTG CCT CCG CGC CCC
Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly>

1250          1260          1270          1280          1290
   *     *       *     *       *     *       *     *       *
TGC GTG TGC CAC CTG CTC ATG GAT GAC GTG GTC AGT GCG GAT AAC TAT
ACG CAC ACG GTG GAC GAG TAC CTA CTG CAC CAG TCA CGC CTA TTG ATA
Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala Asp Asn Tyr>

 1300          1310          1320          1330          1340
    *     *       *     *       *     *       *     *       *
ACA CTG GAC CTG TGG GCT GGG CAG CAG CTG CTG TGG AAG GGC TCC TTC
TGT GAC CTG GAC ACC CGA CCC GTC GTC GAC GAC ACC TTC CCG AGG AAG
Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe>

   1350          1360          1370          1380          1390
*     *       *     *       *     *       *     *       *     *
AAG CCC AGC GAG CAT GTG AAA CCC AGG GCC CCA GGA AAC CTG ACA GTT
TTC GGG TCG CTC GTA CAC TTT GGG TCC CGG GGT CCT TTG GAC TGT CAA
Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn Leu Thr Val>

        1400          1410          1420          1430          1440
    *     *       *     *       *     *       *     *       *     *
CAC ACC AAT GTC TCC GAC ACT CTG CTG CTG ACC TGG AGC AAC CCG TAT
GTG TGG TTA CAG AGG CTG TGA GAC GAC GAC TGG ACC TCG TTG GGC ATA
His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr>

          1450          1460          1470          1480
      *     *       *     *       *     *       *     *     *
CCC CCT GAC AAT TAC CTG TAT AAT CAT CTC ACC TAT GCA GTC AAC ATT
GGG GGA CTG TTA ATG GAC ATA TTA GTA GAG TGG ATA CGT CAG TTG TAA
Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala Val Asn Ile>

1490          1500          1510          1520          1530
   *     *       *     *       *     *       *     *       *
TGG AGT GAA AAC GAC CCG GCA GAT TTC AGA ATC TAT AAC GTG ACC TAC
ACC TCA CTT TTG CTG GGC CGT CTA AAG TCT TAG ATA TTG CAC TGG ATG
Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr>
```

Fig.32E.

```
 1540          1550          1560          1570          1580
    *     *       *     *     *     *       *     *       *
CTA GAA CCC TCC CTC CGC ATC GCA GCC AGC ACC CTG AAG TCT GGG ATT
GAT CTT GGG AGG GAG GCG TAG CGT CGG TCG TGG GAC TTC AGA CCC TAA
Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile>

   1590          1600          1610          1620          1630
*     *       *     *       *     *       *     *       *     *
TCC TAC AGG GCA CGG GTG AGG GCC TGG GCT CAG TGC TAT AAC ACC ACC
AGG ATG TCC CGT GCC CAC TCC CGG ACC CGA GTC ACG ATA TTG TGG TGG
Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr Asn Thr Thr>

      1640          1650          1660          1670          1680
  *       *     *       *     *       *     *       *     *     *
TGG AGT GAG TGG AGC CCC AGC ACC AAG TGG CAC AAC TCC TAC AGG GAG
ACC TCA CTC ACC TCG GGG TCG TGG TTC ACC GTG TTG AGG ATG TCC CTC
Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser Tyr Arg Glu>

         1690          1700          1710          1720
     *       *     *       *     *     *       *     *     *
CCC TTC GAG CAG TCC GGA GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA
GGG AAG CTC GTC AGG CCT CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT
Pro Phe Glu Gln Ser Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro>

1730          1740          1750          1760          1770
  *       *     *       *     *       *     *       *     *     *
GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA
CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys>

 1780          1790          1800          1810          1820
    *     *       *     *       *     *       *     *       *
CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG
GGG TTC CTG TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT ACG CAC
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val>

   1830          1840          1850          1860          1870
*     *       *     *       *     *       *     *       *     *
GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC
CAC CAC CTG CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG TTG ACC ATG
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr>

      1880          1890          1900          1910          1920
  *       *     *       *     *       *     *       *     *     *
GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG
CAC CTG CCG CAC CTC CAC GTA TTA CGG TTC TGT TTC GGC GCC CTC CTC
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu>
```

Fig.32F.

```
          1930          1940          1950          1960
      *     *     *     *     *     *     *     *     *
CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC
GTC ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His>

1970          1980          1990          2000          2010
  *     *     *     *     *     *     *     *     *     *
CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA
GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG TTT
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys>

 2020          2030          2040          2050          2060
    *     *     *     *     *     *     *     *     *
GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG
CGG GAG GGT CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT CCC GTC
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln>

   2070          2080          2090          2100          2110
  *     *     *     *     *     *     *     *     *     *
CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAG GAG ATG
GGG GCT CTT GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC CTC CTC TAC
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met>

       2120          2130          2140          2150          2160
    *     *     *     *     *     *     *     *     *     *
ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC
TGG TTC TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT CCG AAG ATA GGG
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro>

          2170          2180          2190          2200
      *     *     *     *     *     *     *     *     *
AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC
TCG CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn>

2210          2220          2230          2240          2250
  *     *     *     *     *     *     *     *     *     *
TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC
ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG GAG
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu>

 2260          2270          2280          2290          2300
    *     *     *     *     *     *     *     *     *
TAT AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC
ATA TCG TTC GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC TTG CAG
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val>
```

Fig.32G.

```
   2310          2320          2330          2340          2350
*     *       *     *     *       *       *     *       *     *
TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG
AAG AGT ACG AGG CAC TAC GTA CTC CGA GAC GTG TTG GTG ATG TGC GTC
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln>

      2360          2370          2380
  *       *       *     *       *       *
AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA
TTC TCG GAG AGG GAC AGA GGC CCA TTT ACT
Lys Ser Leu Ser Leu Ser Pro Gly Lys ***>
```

Fig.33.

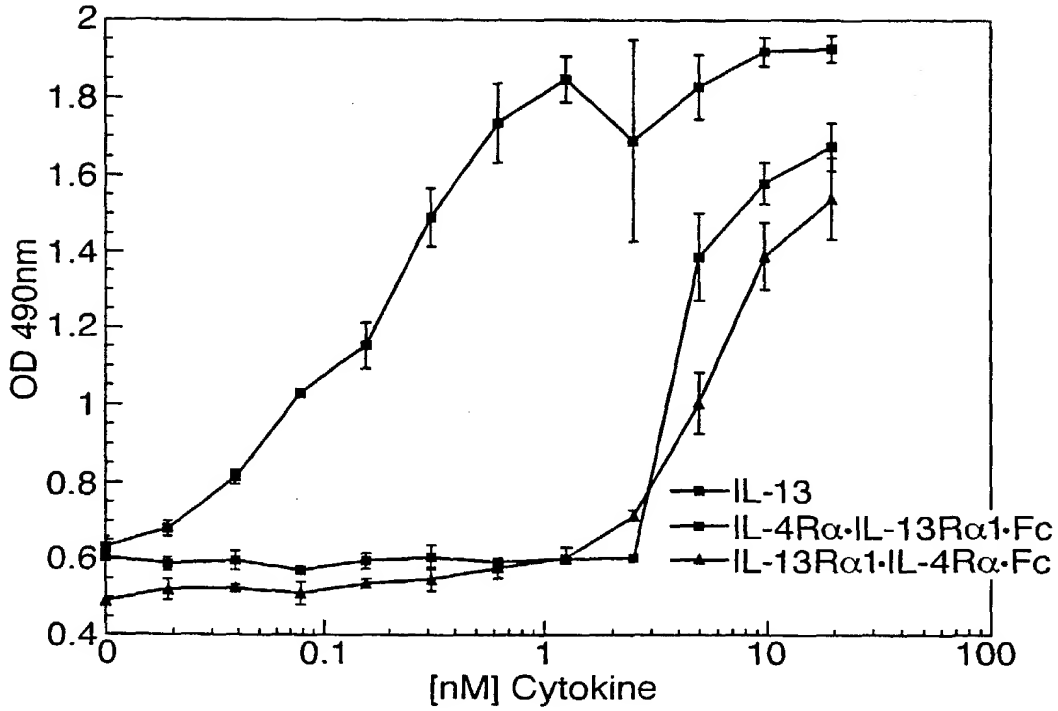
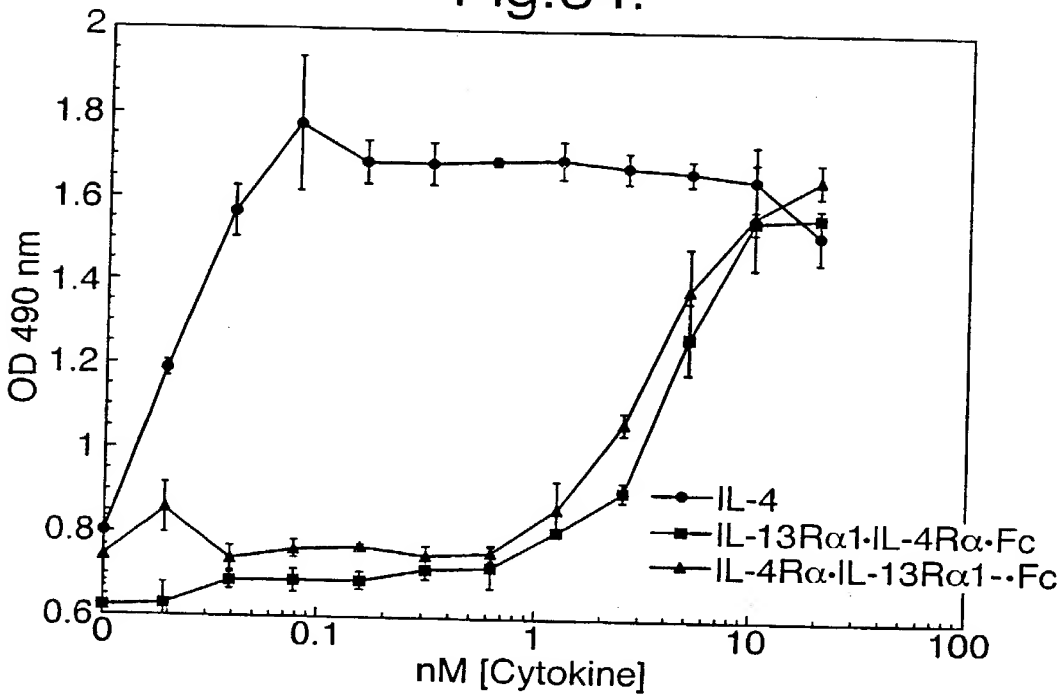


Fig.34.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1.4
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1
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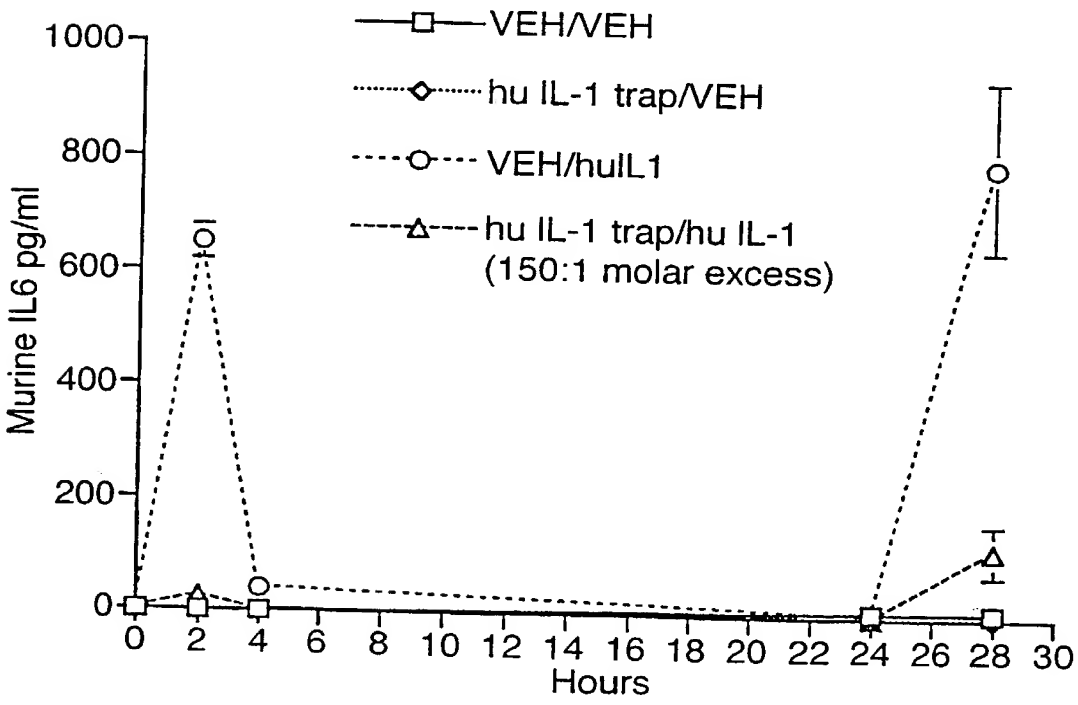
IL-4
IL-13Rα1·IL-4Rα·Fc
IL-4Rα·IL-13Rα1··Fc

Fig.35.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hu IL-1 trap/hu IL-1
(150:1 molar excess)
Murine IL6 pg/ml
1000
800
600
400
200
0
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30
Hours

Fig.36A.

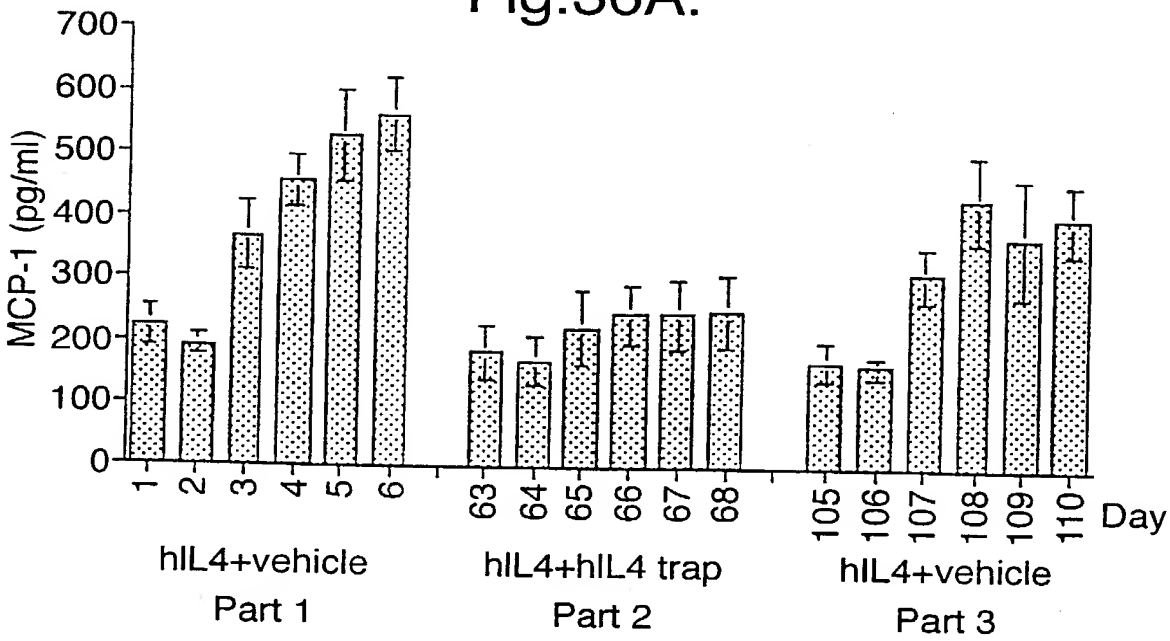


Fig.36B.

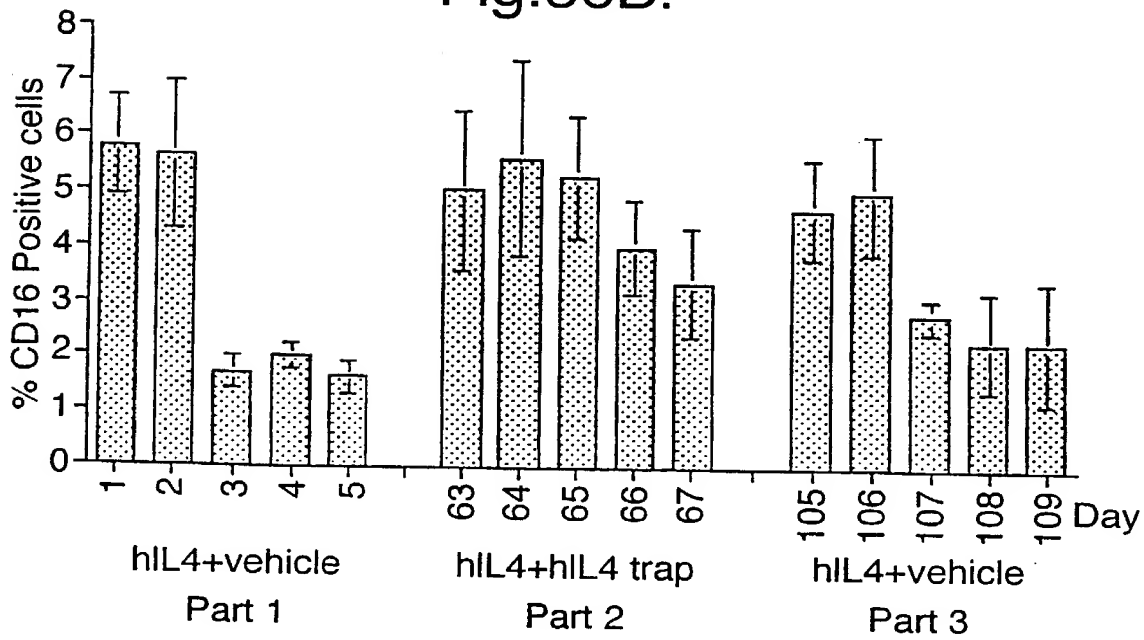
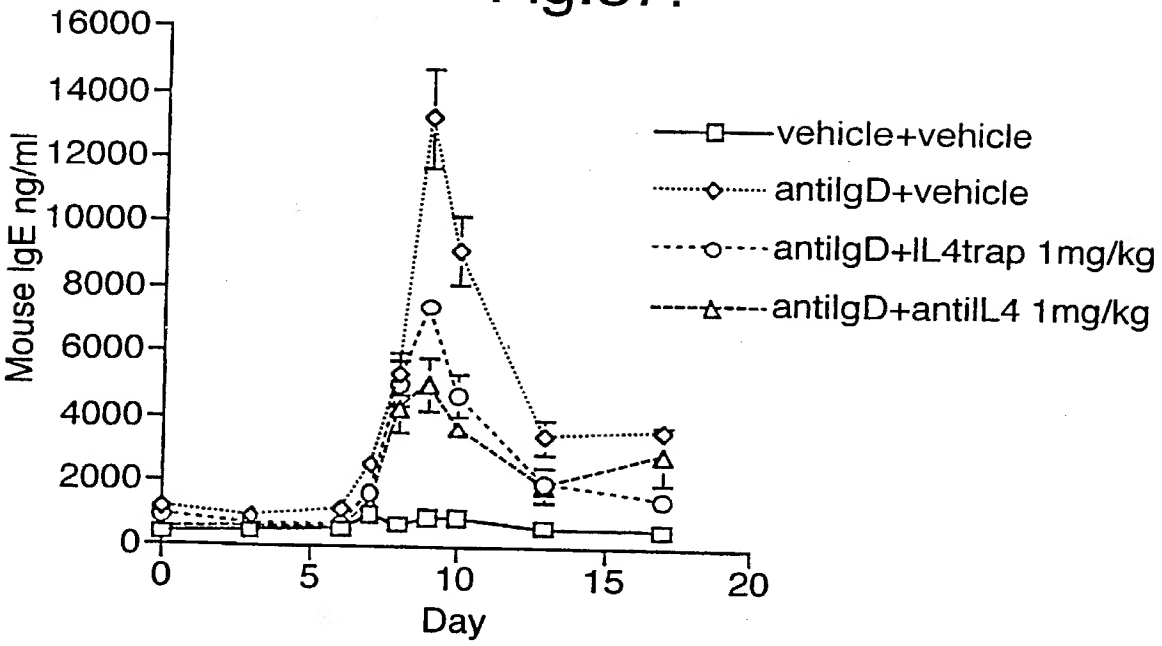


Fig.37.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10
15
20
Day
vehicle+vehicle
antiIgD+vehicle
antiIgD+IL4trap 1mg/kg
antiIgD+antiIL4 1mg/kg

ATT. DOCKET NO. REG 203B-US

DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter that is claimed and for which a patent is sought on the invention entitled **Receptor Based Antagonists, and Methods of Making and Using**, which is the national stage filing of International Application PCT/US99/22045 filed September 22, 1999.

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment specifically referred to in the oath or declaration.

I acknowledge the duty to disclose information of which I am aware that is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §1.56(a).

I hereby claim foreign priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

PCT/US99/22045 filed September 22, 1999.

I hereby claim the benefit under Title 35, United States Code, §119(e) and 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States Application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, §1.56(a) that occurred between the filing date of the prior application and the national or PCT international filing date of this application:

USSN 60/101,858 filed September 25, 1998;
USSN 09/313,942 filed May 19, 1999;

And I hereby appoint Joseph M. Sorrentino (Registration No. 32,598), Gail M. Kempler (Registration No. 32,143), Linda O. Palladino (Registration No. 45,636) and S. Leslie Misrock (Registration No. 18,872), each of them my attorneys and agent, each with full power of substitution and revocation, to prosecute this

application, to make alterations and amendments therein, to receive the patent, to transact all business in the Patent and Trademark Office connected therewith and to file any International Applications that are based thereon under the provisions of the Patent Cooperation Treaty.

Please address all communications, and direct all telephone calls, regarding this application to:

Linda O. Palladino
Regeneron Pharmaceuticals, Inc.
777 Old Saw Mill River Road
Tarrytown, New York 10591
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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

1 – 00

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Signature: [signature] Date: 3/22/01

Citizenship: United States of Ameica

Residence: 1519 Baptist Church Road
Yorktown Heights, New York 10598 NY

Post Office Address: same as residence

SEQUENCE LISTING

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Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
35 40 45
Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
50 55 60
Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
65 70 75 80
Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
85 90 95
Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
100 105 110
Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
115 120 125
Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
130 135 140

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Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
145                 150                 155                 160
Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
                165                 170                 175
Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
            180                 185                 190
Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
        195                 200                 205
Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
    210                 215                 220
Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu
225                 230                 235                 240
Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys
                245                 250                 255
Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
            260                 265                 270
Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
        275                 280                 285
Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu
    290                 295                 300
Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile
305                 310                 315                 320
Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile
                325                 330                 335
Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln Leu Val Trp Lys
            340                 345                 350
Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val
        355                 360                 365
Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Ala
    370                 375                 380
Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu
385                 390                 395                 400
Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala Val Leu Thr Ile
                405                 410                 415
Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala
            420                 425                 430
Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu
        435                 440                 445
Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala
    450                 455                 460
Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr
465                 470                 475                 480
Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val
                485                 490                 495
Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala
            500                 505                 510
Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys
        515                 520                 525
Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val
    530                 535                 540
Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr
545                 550                 555                 560
Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu
                565                 570                 575
Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met
            580                 585                 590
Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe
        595                 600                 605
Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ser Gly Glu Pro Lys
    610                 615                 620
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
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625 630 635 640
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
645 650 655
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
660 665 670
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
675 680 685
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
690 695 700
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
705 710 715 720
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
725 730 735
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
740 745 750
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
755 760 765
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
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785 790 795 800
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
805 810 815
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
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35 40 45
Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
50 55 60
Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
65 70 75 80
Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
85 90 95
Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
100 105 110
Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
115 120 125
Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
130 135 140
Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
145 150 155 160
Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
165 170 175
Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
180 185 190
Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe

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225                 230                 235                 240
Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
                245                 250                 255
Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
            260                 265                 270
Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
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Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
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Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
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Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
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Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
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465                 470                 475                 480
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Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
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Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
        515                 520                 525
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
    530                 535                 540
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
545                 550                 555                 560
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
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Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
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Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
    50                  55                  60
Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
65                  70                  75                  80
Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
                85                  90                  95
Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
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Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
        115                 120                 125
Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
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Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
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Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
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Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile
305                 310                 315                 320
Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile
                325                 330                 335
Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln Leu Val Trp Lys
            340                 345                 350
Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val
        355                 360                 365
Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Ala
    370                 375                 380
Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu
385                 390                 395                 400
Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala Val Leu Thr Ile
                405                 410                 415
Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala
            420                 425                 430
Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu
        435                 440                 445
Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala
    450                 455                 460
Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr
465                 470                 475                 480
Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val
                485                 490                 495
Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala
            500                 505                 510
Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys
        515                 520                 525
```

```
Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val
    530                 535                 540
Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr
545                 550                 555                 560
Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu
                565                 570                 575
Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met
            580                 585                 590
Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe
        595                 600                 605
Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ser Gly Ala Ser Thr
    610                 615                 620
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
625                 630                 635                 640
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                645                 650                 655
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            660                 665                 670
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        675                 680                 685
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    690                 695                 700
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
705                 710                 715                 720
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                725                 730                 735
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            740                 745                 750
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        755                 760                 765
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    770                 775                 780
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
785                 790                 795                 800
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                805                 810                 815
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            820                 825                 830
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        835                 840                 845
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
    850                 855                 860
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
865                 870                 875                 880
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                885                 890                 895
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            900                 905                 910
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        915                 920                 925
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    930                 935                 940
Leu Ser Leu Ser Pro Gly Lys
945                 950
```

<210> 10
<211> 332
<212> PRT
<213> Homo sapiens

<400> 10

```
Met Val Thr Leu Gln Thr Trp Val Val Gln Ala Leu Phe Ile Phe Leu
 1               5                  10                  15
Thr Thr Glu Ser Thr Gly Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser
            20                  25                  30
Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
        35                  40                  45
Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
    50                  55                  60
Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
65                  70                  75                  80
Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
                85                  90                  95
Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
            100                 105                 110
Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
        115                 120                 125
Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
    130                 135                 140
Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
145                 150                 155                 160
Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
                165                 170                 175
Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
            180                 185                 190
Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
        195                 200                 205
Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
    210                 215                 220
Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu
225                 230                 235                 240
Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys
                245                 250                 255
Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
            260                 265                 270
Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
        275                 280                 285
Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu
    290                 295                 300
Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile
305                 310                 315                 320
Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Gly
                325                 330
```

<210> 11
<211> 120
<212> PRT
<213> Homo sapiens

<400> 11

```
Ser Gly Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
 1               5                  10                  15
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
            20                  25                  30
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
        35                  40                  45
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
    50                  55                  60
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
65                  70                  75                  80
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
                85                  90                  95
```

```
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
            100                 105                 110
Lys Ser Cys Asp Lys Thr His Thr
        115                 120

      <210> 12
      <211> 329
      <212> PRT
      <213> Homo sapiens

      <400> 12
Ser Gly Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys
 1               5                  10                  15
Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys
            20                  25                  30
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
        35                  40                  45
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
    50                  55                  60
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
65                  70                  75                  80
Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val
                85                  90                  95
Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
            100                 105                 110
Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        115                 120                 125
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    130                 135                 140
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
145                 150                 155                 160
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                165                 170                 175
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
            180                 185                 190
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        195                 200                 205
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    210                 215                 220
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
225                 230                 235                 240
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                245                 250                 255
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            260                 265                 270
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        275                 280                 285
Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
    290                 295                 300
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
305                 310                 315                 320
Lys Ser Leu Ser Leu Ser Leu Gly Lys
                325

      <210> 13
      <211> 108
      <212> PRT
      <213> Homo sapiens

      <400> 13
Ser Gly Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
```

```
 1               5                  10                  15
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
            20                  25                  30
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
        35                  40                  45
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
    50                  55                  60
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
65                  70                  75                  80
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
                85                  90                  95
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105
```

<210> 14
<211> 106
<212> PRT
<213> Homo sapiens

<400> 14

```
Ser Gly Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 1               5                  10                  15
Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
            20                  25                  30
Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
        35                  40                  45
Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
    50                  55                  60
Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65                  70                  75                  80
Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
                85                  90                  95
Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
            100                 105
```

<210> 15
<211> 360
<212> PRT
<213> Homo sapiens

<400> 15

```
Met Val Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro
 1               5                  10                  15
Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
            20                  25                  30
Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
        35                  40                  45
Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
    50                  55                  60
Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
65                  70                  75                  80
Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
                85                  90                  95
Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
            100                 105                 110
Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
        115                 120                 125
Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
    130                 135                 140
Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
145                 150                 155                 160
```

```
Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
                165                 170                 175
Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
            180                 185                 190
Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
        195                 200                 205
Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val
    210                 215                 220
Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp
225                 230                 235                 240
Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
                245                 250                 255
Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
            260                 265                 270
Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
        275                 280                 285
Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
    290                 295                 300
Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
305                 310                 315                 320
Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr
                325                 330                 335
Asn Lys Asp Asp Asp Asn Ile Leu Phe Arg Asp Ser Ala Asn Ala Thr
            340                 345                 350
Ser Leu Pro Val Gln Asp Ala Gly
        355                 360
```

<210> 16
<211> 315
<212> PRT
<213> Homo sapiens

<400> 16

```
Met Val Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro
 1               5                  10                  15
Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
            20                  25                  30
Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
        35                  40                  45
Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
    50                  55                  60
Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
65                  70                  75                  80
Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
                85                  90                  95
Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
            100                 105                 110
Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
        115                 120                 125
Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
    130                 135                 140
Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
145                 150                 155                 160
Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
                165                 170                 175
Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
            180                 185                 190
Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
        195                 200                 205
Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val
    210                 215                 220
```

```
Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp
225                 230                 235                 240
Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
                245                 250                 255
Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
            260                 265                 270
Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
        275                 280                 285
Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
    290                 295                 300
Glu Trp Ser Pro Glu Ala Met Gly Thr Thr Gly
305                 310                 315
```

<210> 17
<211> 2085
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2082)

<400> 17

```
atg gtg aag cca tca tta cca ttc aca tcc ctc tta ttc ctg cag ctg       48
Met Val Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu
 1               5                  10                  15

ccc ctg ctg gga gtg ggg ctg aac acg aca att ctg acg ccc aat ggg       96
Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly
            20                  25                  30

aat gaa gac acc aca gct gat ttc ttc ctg acc act atg ccc act gac      144
Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp
        35                  40                  45

tcc ctc agt gtt tcc act ctg ccc ctc cca gag gtt cag tgt ttt gtg      192
Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val
    50                  55                  60

ttc aat gtc gag tac atg aat tgc act tgg aac agc agc tct gag ccc      240
Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro
65                  70                  75                  80

cag cct acc aac ctc act ctg cat tat tgg tac aag aac tcg gat aat      288
Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn
                85                  90                  95

gat aaa gtc cag aag tgc agc cac tat cta ttc tct gaa gaa atc act      336
Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr
            100                 105                 110

tct ggc tgt cag ttg caa aaa aag gag atc cac ctc tac caa aca ttt      384
Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe
        115                 120                 125

gtt gtt cag ctc cag gac cca cgg gaa ccc agg aga cag gcc aca cag      432
Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln
    130                 135                 140

atg cta aaa ctg cag aat ctg gtg atc ccc tgg gct cca gag aac cta      480
Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu
```

```
145                 150                 155                 160

aca ctt cac aaa ctg agt gaa tcc cag cta gaa ctg aac tgg aac aac      528
Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn
                165                 170                 175

aga ttc ttg aac cac tgt ttg gag cac ttg gtg cag tac cgg act gac      576
Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp
            180                 185                 190

tgg gac cac agc tgg act gaa caa tca gtg gat tat aga cat aag ttc      624
Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
        195                 200                 205

tcc ttg cct agt gtg gat ggg cag aaa cgc tac acg ttt cgt gtt cgg      672
Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg
    210                 215                 220

agc cgc ttt aac cca ctc tgt gga agt gct cag cat tgg agt gaa tgg      720
Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
225                 230                 235                 240

agc cac cca atc cac tgg ggg agc aat act tca aaa gag aac gcg tcg      768
Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Ala Ser
                245                 250                 255

tct ggg aac atg aag gtc ctg cag gag ccc acc tgc gtc tcc gac tac      816
Ser Gly Asn Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr
            260                 265                 270

atg agc atc tct act tgc gag tgg aag atg aat ggt ccc acc aat tgc      864
Met Ser Ile Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys
        275                 280                 285

agc acc gag ctc cgc ctg ttg tac cag ctg gtt ttt ctg ctc tcc gaa      912
Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu
    290                 295                 300

gcc cac acg tgt atc cct gag aac aac gga ggc gcg ggg tgc gtg tgc      960
Ala His Thr Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys
305                 310                 315                 320

cac ctg ctc atg gat gac gtg gtc agt gcg gat aac tat aca ctg gac     1008
His Leu Leu Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp
                325                 330                 335

ctg tgg gct ggg cag cag ctg ctg tgg aag ggc tcc ttc aag ccc agc     1056
Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser
            340                 345                 350

gag cat gtg aaa ccc agg gcc cca gga aac ctg aca gtt cac acc aat     1104
Glu His Val Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn
        355                 360                 365

gtc tcc gac act ctg ctg ctg acc tgg agc aac ccg tat ccc cct gac     1152
Val Ser Asp Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp
    370                 375                 380

aat tac ctg tat aat cat ctc acc tat gca gtc aac att tgg agt gaa     1200
Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu
385                 390                 395                 400
```

```
aac gac ccg gca gat ttc aga atc tat aac gtg acc tac cta gaa ccc      1248
Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro
                405                 410                 415

tcc ctc cgc atc gca gcc agc acc ctg aag tct ggg att tcc tac agg      1296
Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg
            420                 425                 430

gca cgg gtg agg gcc tgg gct cag tgc tat aac acc acc tgg agt gag      1344
Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr Asn Thr Thr Trp Ser Glu
        435                 440                 445

tgg agc ccc agc acc aag tgg cac aac tcc tac agg gag ccc ttc gag      1392
Trp Ser Pro Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu
    450                 455                 460

cag tcc gga gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa      1440
Gln Ser Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
465                 470                 475                 480

ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac      1488
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                485                 490                 495

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac      1536
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            500                 505                 510

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc      1584
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        515                 520                 525

gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac      1632
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    530                 535                 540

agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg      1680
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
545                 550                 555                 560

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca      1728
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                565                 570                 575

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa      1776
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            580                 585                 590

cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac      1824
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        595                 600                 605

cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc      1872
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    610                 615                 620

gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc      1920
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
625                 630                 635                 640
```

```
acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tat agc aag      1968
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                645                 650                 655

ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc      2016
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        660                 665                 670

tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc      2064
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    675                 680                 685

tcc ctg tct ccg ggt aaa tga                                         2085
Ser Leu Ser Pro Gly Lys
690
```

<210> 18
<211> 694
<212> PRT
<213> Homo sapiens

<400> 18

```
Met Val Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu
 1               5                  10                  15
Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly
            20                  25                  30
Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp
        35                  40                  45
Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val
    50                  55                  60
Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro
65                  70                  75                  80
Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn
                85                  90                  95
Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr
            100                 105                 110
Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe
        115                 120                 125
Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln
    130                 135                 140
Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu
145                 150                 155                 160
Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn
                165                 170                 175
Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp
            180                 185                 190
Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
        195                 200                 205
Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg
    210                 215                 220
Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
225                 230                 235                 240
Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Ala Ser
                245                 250                 255
Ser Gly Asn Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr
            260                 265                 270
Met Ser Ile Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys
        275                 280                 285
Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu
    290                 295                 300
```

```
Ala His Thr Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys
305                 310                 315                 320
His Leu Leu Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp
                325                 330                 335
Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser
            340                 345                 350
Glu His Val Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn
        355                 360                 365
Val Ser Asp Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp
    370                 375                 380
Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu
385                 390                 395                 400
Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro
                405                 410                 415
Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg
            420                 425                 430
Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr Asn Thr Thr Trp Ser Glu
        435                 440                 445
Trp Ser Pro Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu
    450                 455                 460
Gln Ser Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
465                 470                 475                 480
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                485                 490                 495
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            500                 505                 510
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        515                 520                 525
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    530                 535                 540
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
545                 550                 555                 560
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                565                 570                 575
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            580                 585                 590
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        595                 600                 605
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    610                 615                 620
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
625                 630                 635                 640
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                645                 650                 655
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            660                 665                 670
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        675                 680                 685
Ser Leu Ser Pro Gly Lys
    690
```

<210> 19
<211> 2076
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2073)

<400> 19

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atg gtg aag cca tca tta cca ttc aca tcc ctc tta ttc ctg cag ctg        48
Met Val Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu
 1               5                  10                  15

ccc ctg ctg gga gtg ggg ctg aac acg aca att ctg acg ccc aat ggg        96
Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly
            20                  25                  30

aat gaa gac acc aca gct gat ttc ttc ctg acc act atg ccc act gac       144
Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp
        35                  40                  45

tcc ctc agt gtt tcc act ctg ccc ctc cca gag gtt cag tgt ttt gtg       192
Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val
    50                  55                  60

ttc aat gtc gag tac atg aat tgc act tgg aac agc agc tct gag ccc       240
Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro
65                  70                  75                  80

cag cct acc aac ctc act ctg cat tat tgg tac aag aac tcg gat aat       288
Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn
                85                  90                  95

gat aaa gtc cag aag tgc agc cac tat cta ttc tct gaa gaa atc act       336
Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr
            100                 105                 110

tct ggc tgt cag ttg caa aaa aag gag atc cac ctc tac caa aca ttt       384
Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe
        115                 120                 125

gtt gtt cag ctc cag gac cca cgg gaa ccc agg aga cag gcc aca cag       432
Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln
    130                 135                 140

atg cta aaa ctg cag aat ctg gtg atc ccc tgg gct cca gag aac cta       480
Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu
145                 150                 155                 160

aca ctt cac aaa ctg agt gaa tcc cag cta gaa ctg aac tgg aac aac       528
Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn
                165                 170                 175

aga ttc ttg aac cac tgt ttg gag cac ttg gtg cag tac cgg act gac       576
Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp
            180                 185                 190

tgg gac cac agc tgg act gaa caa tca gtg gat tat aga cat aag ttc       624
Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
        195                 200                 205

tcc ttg cct agt gtg gat ggg cag aaa cgc tac acg ttt cgt gtt cgg       672
Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg
    210                 215                 220

agc cgc ttt aac cca ctc tgt gga agt gct cag cat tgg agt gaa tgg       720
Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
225                 230                 235                 240

agc cac cca atc cac tgg ggg agc aat act tca aaa gag aac ggg aac       768
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```
Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Gly Asn
                245                 250                 255

atg aag gtc ctg cag gag ccc acc tgc gtc tcc gac tac atg agc atc      816
Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr Met Ser Ile
            260                 265                 270

tct act tgc gag tgg aag atg aat ggt ccc acc aat tgc agc acc gag      864
Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys Ser Thr Glu
        275                 280                 285

ctc cgc ctg ttg tac cag ctg gtt ttt ctg ctc tcc gaa gcc cac acg      912
Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu Ala His Thr
    290                 295                 300

tgt atc cct gag aac aac gga ggc gcg ggg tgc gtg tgc cac ctg ctc      960
Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys His Leu Leu
305                 310                 315                 320

atg gat gac gtg gtc agt gcg gat aac tat aca ctg gac ctg tgg gct     1008
Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp Leu Trp Ala
                325                 330                 335

ggg cag cag ctg ctg tgg aag ggc tcc ttc aag ccc agc gag cat gtg     1056
Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser Glu His Val
            340                 345                 350

aaa ccc agg gcc cca gga aac ctg aca gtt cac acc aat gtc tcc gac     1104
Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn Val Ser Asp
        355                 360                 365

act ctg ctg ctg acc tgg agc aac ccg tat ccc cct gac aat tac ctg     1152
Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp Asn Tyr Leu
    370                 375                 380

tat aat cat ctc acc tat gca gtc aac att tgg agt gaa aac gac ccg     1200
Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu Asn Asp Pro
385                 390                 395                 400

gca gat ttc aga atc tat aac gtg acc tac cta gaa ccc tcc ctc cgc     1248
Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro Ser Leu Arg
                405                 410                 415

atc gca gcc agc acc ctg aag tct ggg att tcc tac agg gca cgg gtg     1296
Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg Ala Arg Val
            420                 425                 430

agg gcc tgg gct cag agc tat aac acc acc tgg agt gag tgg agc ccc     1344
Arg Ala Trp Ala Gln Ser Tyr Asn Thr Thr Trp Ser Glu Trp Ser Pro
        435                 440                 445

agc acc aag tgg cac aac tcc tac agg gag ccc ttc gag cag tcc gga     1392
Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu Gln Ser Gly
    450                 455                 460

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg     1440
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
465                 470                 475                 480

gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg     1488
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
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                485                 490                 495

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      1536
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            500                 505                 510

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      1584
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        515                 520                 525

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac      1632
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    530                 535                 540

cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc      1680
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
545                 550                 555                 560

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc      1728
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                565                 570                 575

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg      1776
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            580                 585                 590

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc      1824
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        595                 600                 605

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1872
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    610                 615                 620

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc      1920
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
625                 630                 635                 640

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tat agc aag ctc acc gtg      1968
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                645                 650                 655

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg      2016
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            660                 665                 670

cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct      2064
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        675                 680                 685

ccg ggt aaa tga                                                      2076
Pro Gly Lys
    690
```

<210> 20
<211> 691
<212> PRT
<213> Homo sapiens

<400> 20

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Met Val Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu
 1               5                  10                  15
Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly
            20                  25                  30
Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp
        35                  40                  45
Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val
    50                  55                  60
Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro
65                  70                  75                  80
Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn
                85                  90                  95
Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr
            100                 105                 110
Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe
        115                 120                 125
Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln
    130                 135                 140
Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu
145                 150                 155                 160
Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn
                165                 170                 175
Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp
            180                 185                 190
Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
        195                 200                 205
Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg
    210                 215                 220
Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
225                 230                 235                 240
Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Gly Asn
                245                 250                 255
Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr Met Ser Ile
            260                 265                 270
Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys Ser Thr Glu
        275                 280                 285
Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu Ala His Thr
    290                 295                 300
Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys His Leu Leu
305                 310                 315                 320
Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp Leu Trp Ala
                325                 330                 335
Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser Glu His Val
            340                 345                 350
Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn Val Ser Asp
        355                 360                 365
Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp Asn Tyr Leu
    370                 375                 380
Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu Asn Asp Pro
385                 390                 395                 400
Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro Ser Leu Arg
                405                 410                 415
Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg Ala Arg Val
            420                 425                 430
Arg Ala Trp Ala Gln Ser Tyr Asn Thr Thr Trp Ser Glu Trp Ser Pro
        435                 440                 445
Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu Gln Ser Gly
    450                 455                 460
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
465                 470                 475                 480
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
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                485                 490                 495
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            500                 505                 510
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        515                 520                 525
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    530                 535                 540
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
545                 550                 555                 560
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                565                 570                 575
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            580                 585                 590
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        595                 600                 605
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    610                 615                 620
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
625                 630                 635                 640
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                645                 650                 655
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            660                 665                 670
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        675                 680                 685
Pro Gly Lys
    690
```

<210> 21
<211> 2085
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2082)

<400> 21

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atg gtg aag cca tca tta cca ttc aca tcc ctc tta ttc ctg cag ctg        48
Met Val Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu
 1               5                  10                  15

ccc ctg ctg gga gtg ggg ctg aac acg aca att ctg acg ccc aat ggg        96
Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly
            20                  25                  30

aat gaa gac acc aca gct gat ttc ttc ctg acc act atg ccc act gac       144
Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp
        35                  40                  45

tcc ctc agt gtt tcc act ctg ccc ctc cca gag gtt cag tgt ttt gtg       192
Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val
    50                  55                  60

ttc aat gtc gag tac atg aat tgc act tgg aac agc agc tct gag ccc       240
Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro
65                  70                  75                  80

cag cct acc aac ctc act ctg cat tat tgg tac aag aac tcg gat aat       288
Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn
                85                  90                  95
```

```
gat aaa gtc cag aag tgc agc cac tat cta ttc tct gaa gaa atc act      336
Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr
            100                 105                 110

tct ggc tgt cag ttg caa aaa aag gag atc cac ctc tac caa aca ttt      384
Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe
        115                 120                 125

gtt gtt cag ctc cag gac cca cgg gaa ccc agg aga cag gcc aca cag      432
Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln
    130                 135                 140

atg cta aaa ctg cag aat ctg gtg atc ccc tgg gct cca gag aac cta      480
Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu
145                 150                 155                 160

aca ctt cac aaa ctg agt gaa tcc cag cta gaa ctg aac tgg aac aac      528
Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn
                165                 170                 175

aga ttc ttg aac cac tgt ttg gag cac ttg gtg cag tac cgg act gac      576
Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp
            180                 185                 190

tgg gac cac agc tgg act gaa caa tca gtg gat tat aga cat aag ttc      624
Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
        195                 200                 205

tcc ttg cct agt gtg gat ggg cag aaa cgc tac acg ttt cgt gtt cgg      672
Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg
    210                 215                 220

agc cgc ttt aac cca ctc tgt gga agt gct cag cat tgg agt gaa tgg      720
Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
225                 230                 235                 240

agc cac cca atc cac tgg ggg agc aat act tca aaa gag aac gcg tcg      768
Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Ala Ser
                245                 250                 255

tct ggg aac atg aag gtc ctg cag gag ccc acc tgc gtc tcc gac tac      816
Ser Gly Asn Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr
            260                 265                 270

atg agc atc tct act tgc gag tgg aag atg aat ggt ccc acc aat tgc      864
Met Ser Ile Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys
        275                 280                 285

agc acc gag ctc cgc ctg ttg tac cag ctg gtt ttt ctg ctc tcc gaa      912
Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu
    290                 295                 300

gcc cac acg tgt atc cct gag aac aac gga ggc gcg ggg tgc gtg tgc      960
Ala His Thr Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys
305                 310                 315                 320

cac ctg ctc atg gat gac gtg gtc agt gcg gat aac tat aca ctg gac     1008
His Leu Leu Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp
                325                 330                 335
```

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ctg tgg gct ggg cag cag ctg ctg tgg aag ggc tcc ttc aag ccc agc      1056
Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser
            340                 345                 350

gag cat gtg aaa ccc agg gcc cca gga aac ctg aca gtt cac acc aat      1104
Glu His Val Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn
        355                 360                 365

gtc tcc gac act ctg ctg ctg acc tgg agc aac ccg tat ccc cct gac      1152
Val Ser Asp Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp
    370                 375                 380

aat tac ctg tat aat cat ctc acc tat gca gtc aac att tgg agt gaa      1200
Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu
385                 390                 395                 400

aac gac ccg gca gat ttc aga atc tat aac gtg acc tac cta gaa ccc      1248
Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro
                405                 410                 415

tcc ctc cgc atc gca gcc agc acc ctg aag tct ggg att tcc tac agg      1296
Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg
            420                 425                 430

gca cgg gtg agg gcc tgg gct cag agc tat aac acc acc tgg agt gag      1344
Ala Arg Val Arg Ala Trp Ala Gln Ser Tyr Asn Thr Thr Trp Ser Glu
        435                 440                 445

tgg agc ccc agc acc aag tgg cac aac tcc tac agg gag ccc ttc gag      1392
Trp Ser Pro Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu
    450                 455                 460

cag tcc gga gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa      1440
Gln Ser Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
465                 470                 475                 480

ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac      1488
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                485                 490                 495

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac      1536
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            500                 505                 510

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc      1584
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        515                 520                 525

gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac      1632
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    530                 535                 540

agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg      1680
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
545                 550                 555                 560

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca      1728
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                565                 570                 575

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa      1776
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```
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            580                 585                 590

cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac   1824
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
        595                 600                 605

cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc   1872
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    610                 615                 620

gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc   1920
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
625                 630                 635                 640

acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tat agc aag   1968
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                645                 650                 655

ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc   2016
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            660                 665                 670

tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc   2064
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        675                 680                 685

tcc ctg tct ccg ggt aaa tga                                      2085
Ser Leu Ser Pro Gly Lys
    690
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<210> 22
<211> 694
<212> PRT
<213> Homo sapiens

<400> 22

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Met Val Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu
 1               5                  10                  15
Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly
            20                  25                  30
Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp
        35                  40                  45
Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val
    50                  55                  60
Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro
65                  70                  75                  80
Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn
                85                  90                  95
Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr
            100                 105                 110
Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe
        115                 120                 125
Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln
    130                 135                 140
Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu
145                 150                 155                 160
Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn
                165                 170                 175
Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp
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                180                 185                 190
Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
        195                 200                 205
Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg
    210                 215                 220
Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
225                 230                 235                 240
Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Ala Ser
                245                 250                 255
Ser Gly Asn Met Lys Val Leu Gln Glu Pro Thr Cys Val Ser Asp Tyr
            260                 265                 270
Met Ser Ile Ser Thr Cys Glu Trp Lys Met Asn Gly Pro Thr Asn Cys
        275                 280                 285
Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu Leu Ser Glu
    290                 295                 300
Ala His Thr Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly Cys Val Cys
305                 310                 315                 320
His Leu Leu Met Asp Asp Val Val Ser Ala Asp Asn Tyr Thr Leu Asp
                325                 330                 335
Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser
            340                 345                 350
Glu His Val Lys Pro Arg Ala Pro Gly Asn Leu Thr Val His Thr Asn
        355                 360                 365
Val Ser Asp Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp
    370                 375                 380
Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu
385                 390                 395                 400
Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro
                405                 410                 415
Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg
            420                 425                 430
Ala Arg Val Arg Ala Trp Ala Gln Ser Tyr Asn Thr Thr Trp Ser Glu
        435                 440                 445
Trp Ser Pro Ser Thr Lys Trp His Asn Ser Tyr Arg Glu Pro Phe Glu
    450                 455                 460
Gln Ser Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
465                 470                 475                 480
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                485                 490                 495
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            500                 505                 510
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
        515                 520                 525
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
    530                 535                 540
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
545                 550                 555                 560
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
                565                 570                 575
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
            580                 585                 590
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
        595                 600                 605
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    610                 615                 620
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
625                 630                 635                 640
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                645                 650                 655
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
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Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
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Ser Leu Ser Pro Gly Lys
    690
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Met Val Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro
 1               5                  10                  15

gga gcg gcg ctg gcc cca agg cgc tgc cct gcg cag gag gtg gca aga        96
Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
            20                  25                  30

ggc gtg ctg acc agt ctg cca gga gac agc gtg act ctg acc tgc ccg       144
Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
        35                  40                  45

ggg gta gag ccg gaa gac aat gcc act gtt cac tgg gtg ctc agg aag       192
Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
    50                  55                  60

ccg gct gca ggc tcc cac ccc agc aga tgg gct ggc atg gga agg agg       240
Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
65                  70                  75                  80

ctg ctg ctg agg tcg gtg cag ctc cac gac tct gga aac tat tca tgc       288
Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
                85                  90                  95

tac cgg gcc ggc cgc cca gct ggg act gtg cac ttg ctg gtg gat gtt       336
Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
            100                 105                 110

ccc ccc gag gag ccc cag ctc tcc tgc ttc cgg aag agc ccc ctc agc       384
Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
        115                 120                 125

aat gtt gtt tgt gag tgg ggt cct cgg agc acc cca tcc ctg acg aca       432
Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
    130                 135                 140

aag gct gtg ctc ttg gtg agg aag ttt cag aac agt ccg gcc gaa gac       480
Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
145                 150                 155                 160

ttc cag gag ccg tgc cag tat tcc cag gag tcc cag aag ttc tcc tgc       528
Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
                165                 170                 175

cag tta gca gtc ccg gag gga gac agc tct ttc tac ata gtg tcc atg       576
Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
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                180                 185                 190

tgc gtc gcc agt agt gtc ggg agc aag ttc agc aaa act caa acc ttt      624
Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
        195                 200                 205

cag ggt tgt gga atc ttg cag cct gat ccg cct gcc aac atc aca gtc      672
Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val
    210                 215                 220

act gcc gtg gcc aga aac ccc cgc tgg ctc agt gtc acc tgg caa gac      720
Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp
225                 230                 235                 240

ccc cac tcc tgg aac tca tct ttc tac aga cta cgg ttt gag ctc aga      768
Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
                245                 250                 255

tat cgg gct gaa cgg tca aag aca ttc aca aca tgg atg gtc aag gac      816
Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
        260                 265                 270

ctc cag cat cac tgt gtc atc cac gac gcc tgg agc ggc ctg agg cac      864
Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
        275                 280                 285

gtg gtg cag ctt cgt gcc cag gag gag ttc ggg caa ggc gag tgg agc      912
Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
    290                 295                 300

gag tgg agc ccg gag gcc atg ggc acg cct tgg aca gaa tcc agg agt      960
Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
305                 310                 315                 320

cct cca gct gag aac gag gtg tcc acc ccc atg acc ggt ggc gcg cct     1008
Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Thr Gly Gly Ala Pro
                325                 330                 335

tca ggt gct cag ctg gaa ctt cta gac cca tgt ggt tat atc agt cct     1056
Ser Gly Ala Gln Leu Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser Pro
        340                 345                 350

gaa tct cca gtt gta caa ctt cat tct aat ttc act gca gtt tgt gtg     1104
Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys Val
        355                 360                 365

cta aag gaa aaa tgt atg gat tat ttt cat gta aat gct aat tac att     1152
Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr Ile
    370                 375                 380

gtc tgg aaa aca aac cat ttt act att cct aag gag caa tat act atc     1200
Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr Ile
385                 390                 395                 400

ata aac aga aca gca tcc agt gtc acc ttt aca gat ata gct tca tta     1248
Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser Leu
                405                 410                 415

aat att cag ctc act tgc aac att ctt aca ttc gga cag ctt gaa cag     1296
Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu Gln
            420                 425                 430
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aat gtt tat gga atc aca ata att tca ggc ttg cct cca gaa aaa cct      1344
Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys Pro
        435                 440                 445

aaa aat ttg agt tgc att gtg aac gag ggg aag aaa atg agg tgt gag      1392
Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys Glu
    450                 455                 460

tgg gat ggt gga agg gaa aca cac ttg gag aca aac ttc act tta aaa      1440
Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu Lys
465                 470                 475                 480

tct gaa tgg gca aca cac aag ttt gct gat tgc aaa gca aaa cgt gac      1488
Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg Asp
                485                 490                 495

acc ccc acc tca tgc act gtt gat tat tct act gtg tat ttt gtc aac      1536
Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val Asn
            500                 505                 510

att gaa gtc tgg gta gaa gca gag aat gcc ctt ggg aag gtt aca tca      1584
Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr Ser
        515                 520                 525

gat cat atc aat ttt gat cct gta tat aaa gtg aag ccc aat ccg cca      1632
Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro Pro
    530                 535                 540

cat aat tta tca gtg atc aac tca gag gaa ctg tct agt atc tta aaa      1680
His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu Lys
545                 550                 555                 560

ttg aca tgg acc aac cca agt att aag agt gtt ata ata cta aaa tat      1728
Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys Tyr
                565                 570                 575

aac att caa tat agg acc aaa gat gcc tca act tgg agc cag att cct      1776
Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile Pro
            580                 585                 590

cct gaa gac aca gca tcc acc cga tct tca ttc act gtc caa gac ctt      1824
Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp Leu
        595                 600                 605

aaa cct ttt aca gaa tat gtg ttt agg att cgc tgt atg aag gaa gat      1872
Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu Asp
    610                 615                 620

ggt aag gga tac tgg agt gac tgg agt gaa gaa gca agt ggg atc acc      1920
Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile Thr
625                 630                 635                 640

tat gaa gat aga cca tct aaa gca cca agt ttc tgg tat aaa ata gat      1968
Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile Asp
                645                 650                 655

cca tcc cat act caa ggc tac aga act gta caa ctc gtg tgg aag aca      2016
Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln Leu Val Trp Lys Thr
            660                 665                 670
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ttg cct cct ttt gaa gcc aat gga aaa atc ttg gat tat gaa gtg act      2064
Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val Thr
        675                 680                 685

ctc aca aga tgg aaa tca cat tta caa aat tac aca gtt aat gcc aca      2112
Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Ala Thr
    690                 695                 700

aaa ctg aca gta aat ctc aca aat gat cgc tat cta gca acc cta aca      2160
Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu Thr
705                 710                 715                 720

gta aga aat ctt gtt ggc aaa tca gat gca gct gtt tta act atc cct      2208
Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala Val Leu Thr Ile Pro
                725                 730                 735

gcc tgt gac ttt caa gct act cac cct gta atg gat ctt aaa gca ttc      2256
Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala Phe
            740                 745                 750

ccc aaa gat aac atg ctt tgg gtg gaa tgg act act cca agg gaa tct      2304
Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu Ser
        755                 760                 765

gta aag aaa tat ata ctt gag tgg tgt gtg tta tca gat aaa gca ccc      2352
Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala Pro
    770                 775                 780

tgt atc aca gac tgg caa caa gaa gat ggt acc gtg cat cgc acc tat      2400
Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr Tyr
785                 790                 795                 800

tta aga ggg aac tta gca gag agc aaa tgc tat ttg ata aca gtt act      2448
Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val Thr
                805                 810                 815

cca gta tat gct gat gga cca gga agc cct gaa tcc ata aag gca tac      2496
Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala Tyr
            820                 825                 830

ctt aaa caa gct cca cct tcc aaa gga cct act gtt cgg aca aaa aaa      2544
Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys Lys
        835                 840                 845

gta ggg aaa aac gaa gct gtc tta gag tgg gac caa ctt cct gtt gat      2592
Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val Asp
    850                 855                 860

gtt cag aat gga ttt atc aga aat tat act ata ttt tat aga acc atc      2640
Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr Ile
865                 870                 875                 880

att gga aat gaa act gct gtg aat gtg gat tct tcc cac aca gaa tat      2688
Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu Tyr
                885                 890                 895

aca ttg tcc tct ttg act agt gac aca ttg tac atg gta cga atg gca      2736
Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met Ala
            900                 905                 910

gca tac aca gat gaa ggt ggg aag gat ggt cca gaa ttc act ttt act      2784
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Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe Thr
        915                 920                 925

acc cca aag ttt gct caa gga gaa att gaa tcc ggg ggc gac aaa act      2832
Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ser Gly Gly Asp Lys Thr
    930                 935                 940

cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca      2880
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
945                 950                 955                 960

gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg      2928
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                965                 970                 975

acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct      2976
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            980                 985                 990

gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc      3024
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        995                 1000                1005

aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc      3072
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    1010                1015                1020

agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac      3120
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
1025                1030                1035                1040

aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc      3168
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                1045                1050                1055

atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg      3216
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            1060                1065                1070

ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc      3264
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        1075                1080                1085

ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc      3312
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    1090                1095                1100

aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac      3360
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
1105                1110                1115                1120

tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc      3408
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                1125                1130                1135

agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct      3456
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            1140                1145                1150

ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa      3504
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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1155 1160 1165

tga 3507

<210> 24
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<400> 24

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            20                  25                  30
Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
        35                  40                  45
Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
    50                  55                  60
Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
65                  70                  75                  80
Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
                85                  90                  95
Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
            100                 105                 110
Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
        115                 120                 125
Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
    130                 135                 140
Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
145                 150                 155                 160
Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
                165                 170                 175
Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
            180                 185                 190
Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
        195                 200                 205
Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val
    210                 215                 220
Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp
225                 230                 235                 240
Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
                245                 250                 255
Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
            260                 265                 270
Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
        275                 280                 285
Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
    290                 295                 300
Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
305                 310                 315                 320
Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Thr Gly Gly Ala Pro
                325                 330                 335
Ser Gly Ala Gln Leu Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser Pro
            340                 345                 350
Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys Val
        355                 360                 365
Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr Ile
    370                 375                 380
Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr Ile
385                 390                 395                 400
Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser Leu
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                405                 410                 415
Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu Gln
            420                 425                 430
Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys Pro
        435                 440                 445
Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys Glu
    450                 455                 460
Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu Lys
465                 470                 475                 480
Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg Asp
                485                 490                 495
Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val Asn
            500                 505                 510
Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr Ser
        515                 520                 525
Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro Pro
    530                 535                 540
His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu Lys
545                 550                 555                 560
Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys Tyr
                565                 570                 575
Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile Pro
            580                 585                 590
Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp Leu
        595                 600                 605
Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu Asp
    610                 615                 620
Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile Thr
625                 630                 635                 640
Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile Asp
                645                 650                 655
Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln Leu Val Trp Lys Thr
            660                 665                 670
Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val Thr
        675                 680                 685
Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Ala Thr
    690                 695                 700
Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu Thr
705                 710                 715                 720
Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala Val Leu Thr Ile Pro
                725                 730                 735
Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala Phe
            740                 745                 750
Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu Ser
        755                 760                 765
Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala Pro
    770                 775                 780
Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr Tyr
785                 790                 795                 800
Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val Thr
                805                 810                 815
Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala Tyr
            820                 825                 830
Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys Lys
        835                 840                 845
Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val Asp
    850                 855                 860
Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr Ile
865                 870                 875                 880
Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu Tyr
                885                 890                 895
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Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met Ala
            900                 905                 910
Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe Thr
        915                 920                 925
Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ser Gly Gly Asp Lys Thr
    930                 935                 940
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
945                 950                 955                 960
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                965                 970                 975
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            980                 985                 990
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        995                 1000                1005
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    1010                1015                1020
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
1025                1030                1035                1040
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                1045                1050                1055
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            1060                1065                1070
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        1075                1080                1085
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    1090                1095                1100
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
1105                1110                1115                1120
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                1125                1130                1135
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            1140                1145                1150
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        1155                1160                1165
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<210> 25
<211> 3477
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<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(3474)

<400> 25

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atg gtg gcc gtc ggc tgc gcg ctg ctg gct gcc ctg ctg gcc gcg ccg        48
Met Val Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro
 1               5                  10                  15

gga gcg gcg ctg gcc cca agg cgc tgc cct gcg cag gag gtg gca aga        96
Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
            20                  25                  30

ggc gtg ctg acc agt ctg cca gga gac agc gtg act ctg acc tgc ccg       144
Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
        35                  40                  45

ggg gta gag ccg gaa gac aat gcc act gtt cac tgg gtg ctc agg aag       192
Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
    50                  55                  60
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ccg gct gca ggc tcc cac ccc agc aga tgg gct ggc atg gga agg agg      240
Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
 65                  70                  75                  80

ctg ctg ctg agg tcg gtg cag ctc cac gac tct gga aac tat tca tgc      288
Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
                85                  90                  95

tac cgg gcc ggc cgc cca gct ggg act gtg cac ttg ctg gtg gat gtt      336
Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
            100                 105                 110

ccc ccc gag gag ccc cag ctc tcc tgc ttc cgg aag agc ccc ctc agc      384
Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
        115                 120                 125

aat gtt gtt tgt gag tgg ggt cct cgg agc acc cca tcc ctg acg aca      432
Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
    130                 135                 140

aag gct gtg ctc ttg gtg agg aag ttt cag aac agt ccg gcc gaa gac      480
Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
145                 150                 155                 160

ttc cag gag ccg tgc cag tat tcc cag gag tcc cag aag ttc tcc tgc      528
Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
                165                 170                 175

cag tta gca gtc ccg gag gga gac agc tct ttc tac ata gtg tcc atg      576
Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
            180                 185                 190

tgc gtc gcc agt agt gtc ggg agc aag ttc agc aaa act caa acc ttt      624
Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
        195                 200                 205

cag ggt tgt gga atc ttg cag cct gat ccg cct gcc aac atc aca gtc      672
Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val
    210                 215                 220

act gcc gtg gcc aga aac ccc cgc tgg ctc agt gtc acc tgg caa gac      720
Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp
225                 230                 235                 240

ccc cac tcc tgg aac tca tct ttc tac aga cta cgg ttt gag ctc aga      768
Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
                245                 250                 255

tat cgg gct gaa cgg tca aag aca ttc aca aca tgg atg gtc aag gac      816
Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
            260                 265                 270

ctc cag cat cac tgt gtc atc cac gac gcc tgg agc ggc ctg agg cac      864
Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
        275                 280                 285

gtg gtg cag ctt cgt gcc cag gag gag ttc ggg caa ggc gag tgg agc      912
Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
    290                 295                 300

gag tgg agc ccg gag gcc atg ggc acg cct tgg aca gaa tcg cga tcg      960
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Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
305                 310                 315                 320

cct cca gct gag aac gag gtg tcc acc ccc atg gaa ctt cta gac cca      1008
Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Glu Leu Leu Asp Pro
                325                 330                 335

tgt ggt tat atc agt cct gaa tct cca gtt gta caa ctt cat tct aat      1056
Cys Gly Tyr Ile Ser Pro Glu Ser Pro Val Val Gln Leu His Ser Asn
            340                 345                 350

ttc act gca gtt tgt gtg cta aag gaa aaa tgt atg gat tat ttt cat      1104
Phe Thr Ala Val Cys Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His
        355                 360                 365

gta aat gct aat tac att gtc tgg aaa aca aac cat ttt act att cct      1152
Val Asn Ala Asn Tyr Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro
    370                 375                 380

aag gag caa tat act atc ata aac aga aca gca tcc agt gtc acc ttt      1200
Lys Glu Gln Tyr Thr Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe
385                 390                 395                 400

aca gat ata gct tca tta aat att cag ctc act tgc aac att ctt aca      1248
Thr Asp Ile Ala Ser Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr
                405                 410                 415

ttc gga cag ctt gaa cag aat gtt tat gga atc aca ata att tca ggc      1296
Phe Gly Gln Leu Glu Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly
            420                 425                 430

ttg cct cca gaa aaa cct aaa aat ttg agt tgc att gtg aac gag ggg      1344
Leu Pro Pro Glu Lys Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly
        435                 440                 445

aag aaa atg agg tgt gag tgg gat ggt gga agg gaa aca cac ttg gag      1392
Lys Lys Met Arg Cys Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu
    450                 455                 460

aca aac ttc act tta aaa tct gaa tgg gca aca cac aag ttt gct gat      1440
Thr Asn Phe Thr Leu Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp
465                 470                 475                 480

tgc aaa gca aaa cgt gac acc ccc acc tca tgc act gtt gat tat tct      1488
Cys Lys Ala Lys Arg Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser
                485                 490                 495

act gtg tat ttt gtc aac att gaa gtc tgg gta gaa gca gag aat gcc      1536
Thr Val Tyr Phe Val Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala
            500                 505                 510

ctt ggg aag gtt aca tca gat cat atc aat ttt gat cct gta tat aaa      1584
Leu Gly Lys Val Thr Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys
        515                 520                 525

gtg aag ccc aat ccg cca cat aat tta tca gtg atc aac tca gag gaa      1632
Val Lys Pro Asn Pro Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu
    530                 535                 540

ctg tct agt atc tta aaa ttg aca tgg acc aac cca agt att aag agt      1680
Leu Ser Ser Ile Leu Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser
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545                 550                 555                 560

gtt ata ata cta aaa tat aac att caa tat agg acc aaa gat gcc tca      1728
Val Ile Ile Leu Lys Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser
                565                 570                 575

act tgg agc cag att cct cct gaa gac aca gca tcc acc cga tct tca      1776
Thr Trp Ser Gln Ile Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser
            580                 585                 590

ttc act gtc caa gac ctt aaa cct ttt aca gaa tat gtg ttt agg att      1824
Phe Thr Val Gln Asp Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile
        595                 600                 605

cgc tgt atg aag gaa gat ggt aag gga tac tgg agt gac tgg agt gaa      1872
Arg Cys Met Lys Glu Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu
    610                 615                 620

gaa gca agt ggg atc acc tat gaa gat aga cca tct aaa gca cca agt      1920
Glu Ala Ser Gly Ile Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser
625                 630                 635                 640

ttc tgg tat aaa ata gat cca tcc cat act caa ggc tac aga act gta      1968
Phe Trp Tyr Lys Ile Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val
                645                 650                 655

caa ctc gtg tgg aag aca ttg cct cct ttt gaa gcc aat gga aaa atc      2016
Gln Leu Val Trp Lys Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile
            660                 665                 670

ttg gat tat gaa gtg act ctc aca aga tgg aaa tca cat tta caa aat      2064
Leu Asp Tyr Glu Val Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn
        675                 680                 685

tac aca gtt aat gcc aca aaa ctg aca gta aat ctc aca aat gat cgc      2112
Tyr Thr Val Asn Ala Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg
    690                 695                 700

tat cta gca acc cta aca gta aga aat ctt gtt ggc aaa tca gat gca      2160
Tyr Leu Ala Thr Leu Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala
705                 710                 715                 720

gct gtt tta act atc cct gcc tgt gac ttt caa gct act cac cct gta      2208
Ala Val Leu Thr Ile Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val
                725                 730                 735

atg gat ctt aaa gca ttc ccc aaa gat aac atg ctt tgg gtg gaa tgg      2256
Met Asp Leu Lys Ala Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp
            740                 745                 750

act act cca agg gaa tct gta aag aaa tat ata ctt gag tgg tgt gtg      2304
Thr Thr Pro Arg Glu Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val
        755                 760                 765

tta tca gat aaa gca ccc tgt atc aca gac tgg caa caa gaa gat ggt      2352
Leu Ser Asp Lys Ala Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly
    770                 775                 780

acc gtg cat cgc acc tat tta aga ggg aac tta gca gag agc aaa tgc      2400
Thr Val His Arg Thr Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys
785                 790                 795                 800
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```
tat ttg ata aca gtt act cca gta tat gct gat gga cca gga agc cct      2448
Tyr Leu Ile Thr Val Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro
                805                 810                 815

gaa tcc ata aag gca tac ctt aaa caa gct cca cct tcc aaa gga cct      2496
Glu Ser Ile Lys Ala Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro
            820                 825                 830

act gtt cgg aca aaa aaa gta ggg aaa aac gaa gct gtc tta gag tgg      2544
Thr Val Arg Thr Lys Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp
        835                 840                 845

gac caa ctt cct gtt gat gtt cag aat gga ttt atc aga aat tat act      2592
Asp Gln Leu Pro Val Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr
    850                 855                 860

ata ttt tat aga acc atc att gga aat gaa act gct gtg aat gtg gat      2640
Ile Phe Tyr Arg Thr Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp
865                 870                 875                 880

tct tcc cac aca gaa tat aca ttg tcc tct ttg act agt gac aca ttg      2688
Ser Ser His Thr Glu Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu
                885                 890                 895

tac atg gta cga atg gca gca tac aca gat gaa ggt ggg aag gat ggt      2736
Tyr Met Val Arg Met Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly
            900                 905                 910

cca gaa ttc act ttt act acc cca aag ttt gct caa gga gaa att gaa      2784
Pro Glu Phe Thr Phe Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu
        915                 920                 925

tcc ggg ggc gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa      2832
Ser Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
    930                 935                 940

ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac      2880
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
945                 950                 955                 960

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac      2928
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
                965                 970                 975

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc      2976
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
            980                 985                 990

gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac      3024
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
        995                 1000                1005

agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg      3072
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
    1010                1015                1020

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca      3120
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
1025                1030                1035                1040
```

```
gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa      3168
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
                1045                1050                1055

cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac      3216
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
            1060                1065                1070

cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc      3264
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
        1075                1080                1085

gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc      3312
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
    1090                1095                1100

acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag      3360
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
1105                1110                1115                1120

ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc      3408
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
                1125                1130                1135

tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc      3456
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
            1140                1145                1150

tcc ctg tct ccg ggt aaa tga                                         3477
Ser Leu Ser Pro Gly Lys
        1155
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<210> 26
<211> 1158
<212> PRT
<213> Homo sapiens

<400> 26

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Met Val Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro
 1               5                  10                  15
Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
            20                  25                  30
Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
        35                  40                  45
Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
    50                  55                  60
Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
65                  70                  75                  80
Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
                85                  90                  95
Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
            100                 105                 110
Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
        115                 120                 125
Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
    130                 135                 140
Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
145                 150                 155                 160
Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
                165                 170                 175
```

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Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
            180                 185                 190
Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
        195                 200                 205
Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val
    210                 215                 220
Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp
225                 230                 235                 240
Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
                245                 250                 255
Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
            260                 265                 270
Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
        275                 280                 285
Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
    290                 295                 300
Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
305                 310                 315                 320
Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Glu Leu Leu Asp Pro
                325                 330                 335
Cys Gly Tyr Ile Ser Pro Glu Ser Pro Val Val Gln Leu His Ser Asn
            340                 345                 350
Phe Thr Ala Val Cys Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His
        355                 360                 365
Val Asn Ala Asn Tyr Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro
    370                 375                 380
Lys Glu Gln Tyr Thr Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe
385                 390                 395                 400
Thr Asp Ile Ala Ser Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr
                405                 410                 415
Phe Gly Gln Leu Glu Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly
            420                 425                 430
Leu Pro Pro Glu Lys Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly
        435                 440                 445
Lys Lys Met Arg Cys Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu
    450                 455                 460
Thr Asn Phe Thr Leu Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp
465                 470                 475                 480
Cys Lys Ala Lys Arg Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser
                485                 490                 495
Thr Val Tyr Phe Val Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala
            500                 505                 510
Leu Gly Lys Val Thr Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys
        515                 520                 525
Val Lys Pro Asn Pro Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu
    530                 535                 540
Leu Ser Ser Ile Leu Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser
545                 550                 555                 560
Val Ile Ile Leu Lys Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser
                565                 570                 575
Thr Trp Ser Gln Ile Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser
            580                 585                 590
Phe Thr Val Gln Asp Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile
        595                 600                 605
Arg Cys Met Lys Glu Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu
    610                 615                 620
Glu Ala Ser Gly Ile Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser
625                 630                 635                 640
Phe Trp Tyr Lys Ile Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val
                645                 650                 655
Gln Leu Val Trp Lys Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile
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                660                 665                 670
Leu Asp Tyr Glu Val Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn
        675                 680                 685
Tyr Thr Val Asn Ala Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg
    690                 695                 700
Tyr Leu Ala Thr Leu Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala
705                 710                 715                 720
Ala Val Leu Thr Ile Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val
                725                 730                 735
Met Asp Leu Lys Ala Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp
            740                 745                 750
Thr Thr Pro Arg Glu Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val
        755                 760                 765
Leu Ser Asp Lys Ala Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly
    770                 775                 780
Thr Val His Arg Thr Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys
785                 790                 795                 800
Tyr Leu Ile Thr Val Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro
                805                 810                 815
Glu Ser Ile Lys Ala Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro
            820                 825                 830
Thr Val Arg Thr Lys Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp
        835                 840                 845
Asp Gln Leu Pro Val Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr
    850                 855                 860
Ile Phe Tyr Arg Thr Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp
865                 870                 875                 880
Ser Ser His Thr Glu Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu
                885                 890                 895
Tyr Met Val Arg Met Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly
            900                 905                 910
Pro Glu Phe Thr Phe Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu
        915                 920                 925
Ser Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
    930                 935                 940
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
945                 950                 955                 960
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
                965                 970                 975
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
            980                 985                 990
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
        995                 1000                1005
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
    1010                1015                1020
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
1025                1030                1035                1040
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
                1045                1050                1055
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
            1060                1065                1070
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
        1075                1080                1085
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
    1090                1095                1100
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
1105                1110                1115                1120
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
                1125                1130                1135
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
            1140                1145                1150
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Ser Leu Ser Pro Gly Lys
        1155

      <210> 27
      <211> 2733
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (1)...(2730)

      <400> 27
atg gtg ctt ctg tgg tgt gta gtg agt ctc tac ttt tat gga atc ctg        48
Met Val Leu Leu Trp Cys Val Val Ser Leu Tyr Phe Tyr Gly Ile Leu
 1               5                  10                  15

caa agt gat gcc tca gaa cgc tgc gat gac tgg gga cta gac acc atg        96
Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
            20                  25                  30

agg caa atc caa gtg ttt gaa gat gag cca gct cgc atc aag tgc cca       144
Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
        35                  40                  45

ctc ttt gaa cac ttc ttg aaa ttc aac tac agc aca gcc cat tca gct       192
Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala
    50                  55                  60

ggc ctt act ctg atc tgg tat tgg act agg cag gac cgg gac ctt gag       240
Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
65                  70                  75                  80

gag cca att aac ttc cgc ctc ccc gag aac cgc att agt aag gag aaa       288
Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
                85                  90                  95

gat gtg ctg tgg ttc cgg ccc act ctc ctc aat gac act ggc aac tat       336
Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
            100                 105                 110

acc tgc atg tta agg aac act aca tat tgc agc aaa gtt gca ttt ccc       384
Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
        115                 120                 125

ttg gaa gtt gtt caa aaa gac agc tgt ttc aat tcc ccc atg aaa ctc       432
Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu
    130                 135                 140

cca gtg cat aaa ctg tat ata gaa tat ggc att cag agg atc act tgt       480
Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys
145                 150                 155                 160

cca aat gta gat gga tat ttt cct tcc agt gtc aaa ccg act atc act       528
Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr
                165                 170                 175

tgg tat atg ggc tgt tat aaa ata cag aat ttt aat aat gta ata ccc       576
Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro
            180                 185                 190
```

```
gaa ggt atg aac ttg agt ttc ctc att gcc tta att tca aat aat gga      624
Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly
        195                 200                 205

aat tac aca tgt gtt gtt aca tat cca gaa aat gga cgt acg ttt cat      672
Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His
    210                 215                 220

ctc acc agg act ctg act gta aag gta gta ggc tct cca aaa aat gca      720
Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala
225                 230                 235                 240

gtg ccc cct gtg atc cat tca cct aat gat cat gtg gtc tat gag aaa      768
Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys
                245                 250                 255

gaa cca gga gag gag cta ctc att ccc tgt acg gtc tat ttt agt ttt      816
Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe
            260                 265                 270

ctg atg gat tct cgc aat gag gtt tgg tgg acc att gat gga aaa aaa      864
Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
        275                 280                 285

cct gat gac atc act att gat gtc acc att aac gaa agt ata agt cat      912
Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His
    290                 295                 300

agt aga aca gaa gat gaa aca aga act cag att ttg agc atc aag aaa      960
Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
305                 310                 315                 320

gtt acc tct gag gat ctc aag cgc agc tat gtc tgt cat gct aga agt     1008
Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser
                325                 330                 335

gcc aaa ggc gaa gtt gcc aaa gca gcc aag gtg aag cag aaa gtg cca     1056
Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro
            340                 345                 350

gct cca aga tac aca gtg tcc ggt ggc gcg cct atg ctg agc gag gct     1104
Ala Pro Arg Tyr Thr Val Ser Gly Gly Ala Pro Met Leu Ser Glu Ala
        355                 360                 365

gat aaa tgc aag gaa cgt gaa gaa aaa ata att tta gtg tca tct gca     1152
Asp Lys Cys Lys Glu Arg Glu Glu Lys Ile Ile Leu Val Ser Ser Ala
    370                 375                 380

aat gaa att gat gtt cgt ccc tgt cct ctt aac cca aat gaa cac aaa     1200
Asn Glu Ile Asp Val Arg Pro Cys Pro Leu Asn Pro Asn Glu His Lys
385                 390                 395                 400

ggc act ata act tgg tat aag gat gac agc aag aca cct gta tct aca     1248
Gly Thr Ile Thr Trp Tyr Lys Asp Asp Ser Lys Thr Pro Val Ser Thr
                405                 410                 415

gaa caa gcc tcc agg att cat caa cac aaa gag aaa ctt tgg ttt gtt     1296
Glu Gln Ala Ser Arg Ile His Gln His Lys Glu Lys Leu Trp Phe Val
            420                 425                 430

cct gct aag gtg gag gat tca gga cat tac tat tgc gtg gta aga aat     1344
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Pro Ala Lys Val Glu Asp Ser Gly His Tyr Tyr Cys Val Val Arg Asn
        435                 440                 445

tca tct tac tgc ctc aga att aaa ata agt gca aaa ttt gtg gag aat      1392
Ser Ser Tyr Cys Leu Arg Ile Lys Ile Ser Ala Lys Phe Val Glu Asn
    450                 455                 460

gag cct aac tta tgt tat aat gca caa gcc ata ttt aag cag aaa cta      1440
Glu Pro Asn Leu Cys Tyr Asn Ala Gln Ala Ile Phe Lys Gln Lys Leu
465                 470                 475                 480

ccc gtt gca gga gac gga gga ctt gtg tgc cct tat atg gag ttt ttt      1488
Pro Val Ala Gly Asp Gly Gly Leu Val Cys Pro Tyr Met Glu Phe Phe
                485                 490                 495

aaa aat gaa aat aat gag tta cct aaa tta cag tgg tat aag gat tgc      1536
Lys Asn Glu Asn Asn Glu Leu Pro Lys Leu Gln Trp Tyr Lys Asp Cys
            500                 505                 510

aaa cct cta ctt ctt gac aat ata cac ttt agt gga gtc aaa gat agg      1584
Lys Pro Leu Leu Leu Asp Asn Ile His Phe Ser Gly Val Lys Asp Arg
        515                 520                 525

ctc atc gtg atg aat gtg gct gaa aag cat aga ggg aac tat act tgt      1632
Leu Ile Val Met Asn Val Ala Glu Lys His Arg Gly Asn Tyr Thr Cys
    530                 535                 540

cat gca tcc tac aca tac ttg ggc aag caa tat cct att acc cgg gta      1680
His Ala Ser Tyr Thr Tyr Leu Gly Lys Gln Tyr Pro Ile Thr Arg Val
545                 550                 555                 560

ata gaa ttt att act cta gag gaa aac aaa ccc aca agg cct gtg att      1728
Ile Glu Phe Ile Thr Leu Glu Glu Asn Lys Pro Thr Arg Pro Val Ile
                565                 570                 575

gtg agc cca gct aat gag aca atg gaa gta gac ttg gga tcc cag ata      1776
Val Ser Pro Ala Asn Glu Thr Met Glu Val Asp Leu Gly Ser Gln Ile
            580                 585                 590

caa ttg atc tgt aat gtc acc ggc cag ttg agt gac att gct tac tgg      1824
Gln Leu Ile Cys Asn Val Thr Gly Gln Leu Ser Asp Ile Ala Tyr Trp
        595                 600                 605

aag tgg aat ggg tca gta att gat gaa gat gac cca gtg cta ggg gaa      1872
Lys Trp Asn Gly Ser Val Ile Asp Glu Asp Asp Pro Val Leu Gly Glu
    610                 615                 620

gac tat tac agt gtg gaa aat cct gca aac aaa aga agg agt acc ctc      1920
Asp Tyr Tyr Ser Val Glu Asn Pro Ala Asn Lys Arg Arg Ser Thr Leu
625                 630                 635                 640

atc aca gtg ctt aat ata tcg gaa att gag agt aga ttt tat aaa cat      1968
Ile Thr Val Leu Asn Ile Ser Glu Ile Glu Ser Arg Phe Tyr Lys His
                645                 650                 655

cca ttt acc tgt ttt gcc aag aat aca cat ggt ata gat gca gca tat      2016
Pro Phe Thr Cys Phe Ala Lys Asn Thr His Gly Ile Asp Ala Ala Tyr
            660                 665                 670

atc cag tta ata tat cca gtc act aat tcc gga gac aaa act cac aca      2064
Ile Gln Leu Ile Tyr Pro Val Thr Asn Ser Gly Asp Lys Thr His Thr
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        675                 680                 685

tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc      2112
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
    690                 695                 700

ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct      2160
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
705                 710                 715                 720

gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc      2208
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
                725                 730                 735

aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca      2256
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
            740                 745                 750

aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc      2304
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
        755                 760                 765

ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc      2352
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
    770                 775                 780

aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc      2400
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
785                 790                 795                 800

aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca      2448
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
                805                 810                 815

tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc ctg gtc      2496
Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
            820                 825                 830

aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg      2544
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
        835                 840                 845

cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac      2592
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
    850                 855                 860

ggc tcc ttc ttc ctc tat agc aag ctc acc gtg gac aag agc agg tgg      2640
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
865                 870                 875                 880

cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac      2688
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
                885                 890                 895

aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa              2730
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            900                 905                 910

tga                                                                  2733
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<210> 28

<211> 910
<212> PRT
<213> Homo sapiens

<400> 28

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Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
            20                  25                  30
Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
        35                  40                  45
Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala
    50                  55                  60
Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
65                  70                  75                  80
Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
                85                  90                  95
Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
            100                 105                 110
Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
        115                 120                 125
Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu
    130                 135                 140
Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys
145                 150                 155                 160
Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr
                165                 170                 175
Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro
            180                 185                 190
Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly
        195                 200                 205
Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His
    210                 215                 220
Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala
225                 230                 235                 240
Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys
                245                 250                 255
Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe
            260                 265                 270
Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
        275                 280                 285
Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His
    290                 295                 300
Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
305                 310                 315                 320
Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser
                325                 330                 335
Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro
            340                 345                 350
Ala Pro Arg Tyr Thr Val Ser Gly Gly Ala Pro Met Leu Ser Glu Ala
        355                 360                 365
Asp Lys Cys Lys Glu Arg Glu Glu Lys Ile Ile Leu Val Ser Ser Ala
    370                 375                 380
Asn Glu Ile Asp Val Arg Pro Cys Pro Leu Asn Pro Asn Glu His Lys
385                 390                 395                 400
Gly Thr Ile Thr Trp Tyr Lys Asp Asp Ser Lys Thr Pro Val Ser Thr
                405                 410                 415
Glu Gln Ala Ser Arg Ile His Gln His Lys Glu Lys Leu Trp Phe Val
            420                 425                 430
Pro Ala Lys Val Glu Asp Ser Gly His Tyr Tyr Cys Val Val Arg Asn
        435                 440                 445
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Ser Ser Tyr Cys Leu Arg Ile Lys Ile Ser Ala Lys Phe Val Glu Asn
    450                 455                 460
Glu Pro Asn Leu Cys Tyr Asn Ala Gln Ala Ile Phe Lys Gln Lys Leu
465                 470                 475                 480
Pro Val Ala Gly Asp Gly Gly Leu Val Cys Pro Tyr Met Glu Phe Phe
                485                 490                 495
Lys Asn Glu Asn Asn Glu Leu Pro Lys Leu Gln Trp Tyr Lys Asp Cys
            500                 505                 510
Lys Pro Leu Leu Leu Asp Asn Ile His Phe Ser Gly Val Lys Asp Arg
        515                 520                 525
Leu Ile Val Met Asn Val Ala Glu Lys His Arg Gly Asn Tyr Thr Cys
    530                 535                 540
His Ala Ser Tyr Thr Tyr Leu Gly Lys Gln Tyr Pro Ile Thr Arg Val
545                 550                 555                 560
Ile Glu Phe Ile Thr Leu Glu Glu Asn Lys Pro Thr Arg Pro Val Ile
                565                 570                 575
Val Ser Pro Ala Asn Glu Thr Met Glu Val Asp Leu Gly Ser Gln Ile
            580                 585                 590
Gln Leu Ile Cys Asn Val Thr Gly Gln Leu Ser Asp Ile Ala Tyr Trp
        595                 600                 605
Lys Trp Asn Gly Ser Val Ile Asp Glu Asp Asp Pro Val Leu Gly Glu
    610                 615                 620
Asp Tyr Tyr Ser Val Glu Asn Pro Ala Asn Lys Arg Arg Ser Thr Leu
625                 630                 635                 640
Ile Thr Val Leu Asn Ile Ser Glu Ile Glu Ser Arg Phe Tyr Lys His
                645                 650                 655
Pro Phe Thr Cys Phe Ala Lys Asn Thr His Gly Ile Asp Ala Ala Tyr
            660                 665                 670
Ile Gln Leu Ile Tyr Pro Val Thr Asn Ser Gly Asp Lys Thr His Thr
        675                 680                 685
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
    690                 695                 700
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
705                 710                 715                 720
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
                725                 730                 735
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
            740                 745                 750
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
        755                 760                 765
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
    770                 775                 780
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
785                 790                 795                 800
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
                805                 810                 815
Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
            820                 825                 830
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
        835                 840                 845
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
    850                 855                 860
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
865                 870                 875                 880
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
                885                 890                 895
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            900                 905                 910
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<210> 29
<211> 2355

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2352)

<400> 29

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Met Val Trp Leu Cys Ser Gly Leu Leu Phe Pro Val Ser Cys Leu Val
 1               5                  10                  15

ctg ctg cag gtg gca agc tct ggg aac atg aag gtc ttg cag gag ccc        96
Leu Leu Gln Val Ala Ser Ser Gly Asn Met Lys Val Leu Gln Glu Pro
            20                  25                  30

acc tgc gtc tcc gac tac atg agc atc tct act tgc gag tgg aag atg       144
Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met
        35                  40                  45

aat ggt ccc acc aat tgc agc acc gag ctc cgc ctg ttg tac cag ctg       192
Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu
    50                  55                  60

gtt ttt ctg ctc tcc gaa gcc cac acg tgt atc cct gag aac aac gga       240
Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly
65                  70                  75                  80

ggc gcg ggg tgc gtg tgc cac ctg ctc atg gat gac gtg gtc agt gcg       288
Gly Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala
                85                  90                  95

gat aac tat aca ctg gac ctg tgg gct ggg cag cag ctg ctg tgg aag       336
Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys
            100                 105                 110

ggc tcc ttc aag ccc agc gag cat gtg aaa ccc agg gcc cca gga aac       384
Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn
        115                 120                 125

ctg aca gtt cac acc aat gtc tcc gac act ctg ctg ctg acc tgg agc       432
Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser
    130                 135                 140

aac ccg tat ccc cct gac aat tac ctg tat aat cat ctc acc tat gca       480
Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala
145                 150                 155                 160

gtc aac att tgg agt gaa aac gac ccg gca gat ttc aga atc tat aac       528
Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn
                165                 170                 175

gtg acc tac cta gaa ccc tcc ctc cgc atc gca gcc agc acc ctg aag       576
Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys
            180                 185                 190

tct ggg att tcc tac agg gca cgg gtg agg gcc tgg gct cag agc tat       624
Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Ser Tyr
        195                 200                 205

aac acc acc tgg agt gag tgg agc ccc agc acc aag tgg cac aac tcc       672
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Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser
    210                 215                 220

tac agg gag ccc ttc gag cag tcc ggt ggg ggc ggg ggc gcc gcg cct      720
Tyr Arg Glu Pro Phe Glu Gln Ser Gly Gly Gly Gly Gly Ala Ala Pro
225                 230                 235                 240

acg gaa act cag cca cct gtg aca aat ttg agt gtc tct gtt gaa aac      768
Thr Glu Thr Gln Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn
                245                 250                 255

ctc tgc aca gta ata tgg aca tgg aat cca ccc gag gga gcc agc tca      816
Leu Cys Thr Val Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser
            260                 265                 270

aat tgt agt cta tgg tat ttt agt cat ttt ggc gac aaa caa gat aag      864
Asn Cys Ser Leu Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys
        275                 280                 285

aaa ata gct ccg gaa act cgt cgt tca ata gaa gta ccc ctg aat gag      912
Lys Ile Ala Pro Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu
    290                 295                 300

agg att tgt ctg caa gtg ggg tcc cag tgt agc acc aat gag agt gag      960
Arg Ile Cys Leu Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu
305                 310                 315                 320

aag cct agc att ttg gtt gaa aaa tgc atc tca ccc cca gaa ggt gat     1008
Lys Pro Ser Ile Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp
                325                 330                 335

cct gag tct gct gtg act gag ctt caa tgc att tgg cac aac ctg agc     1056
Pro Glu Ser Ala Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser
            340                 345                 350

tac atg aag tgt tct tgg ctc cct gga agg aat acc agt ccc gac act     1104
Tyr Met Lys Cys Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr
        355                 360                 365

aac tat act ctc tac tat tgg cac aga agc ctg gaa aaa att cat caa     1152
Asn Tyr Thr Leu Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln
    370                 375                 380

tgt gaa aac atc ttt aga gaa ggc caa tac ttt ggt tgt tcc ttt gat     1200
Cys Glu Asn Ile Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp
385                 390                 395                 400

ctg acc aaa gtg aag gat tcc agt ttt gaa caa cac agt gtc caa ata     1248
Leu Thr Lys Val Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile
                405                 410                 415

atg gtc aag gat aat gca gga aaa att aaa cca tcc ttc aat ata gtg     1296
Met Val Lys Asp Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val
            420                 425                 430

cct tta act tcc cgt gtg aaa cct gat cct cca cat att aaa aac ctc     1344
Pro Leu Thr Ser Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu
        435                 440                 445

tcc ttc cac aat gat gac cta tat gtg caa tgg gag aat cca cag aat     1392
Ser Phe His Asn Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn
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    450                 455                 460

ttt att agc aga tgc cta ttt tat gaa gta gaa gtc aat aac agc caa      1440
Phe Ile Ser Arg Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln
465                 470                 475                 480

act gag aca cat aat gtt ttc tac gtc caa gag gct aaa tgt gag aat      1488
Thr Glu Thr His Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn
                485                 490                 495

cca gaa ttt gag aga aat gtg gag aat aca tct tgt ttc atg gtc cct      1536
Pro Glu Phe Glu Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro
            500                 505                 510

ggt gtt ctt cct gat act ttg aac aca gtc aga ata aga gtc aaa aca      1584
Gly Val Leu Pro Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr
        515                 520                 525

aat aag tta tgc tat gag gat gac aaa ctc tgg agt aat tgg agc caa      1632
Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln
    530                 535                 540

gaa atg agt ata ggt aag aag cgc aat tcc aca acc gga gac aaa act      1680
Glu Met Ser Ile Gly Lys Lys Arg Asn Ser Thr Thr Gly Asp Lys Thr
545                 550                 555                 560

cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca      1728
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
                565                 570                 575

gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg      1776
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
            580                 585                 590

acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct      1824
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
        595                 600                 605

gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc      1872
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
    610                 615                 620

aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc      1920
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
625                 630                 635                 640

agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac      1968
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
                645                 650                 655

aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc      2016
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
            660                 665                 670

atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg      2064
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
        675                 680                 685

ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc      2112
Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
    690                 695                 700
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ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc      2160
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
705                 710                 715                 720

aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac      2208
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
                725                 730                 735

tcc gac ggc tcc ttc ttc ctc tat agc aag ctc acc gtg gac aag agc      2256
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
            740                 745                 750

agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct      2304
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
        755                 760                 765

ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa      2352
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    770                 775                 780

tga                                                                 2355
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<210> 30
<211> 784
<212> PRT
<213> Homo sapiens

<400> 30

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            20                  25                  30
Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met
        35                  40                  45
Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu
    50                  55                  60
Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly
65                  70                  75                  80
Gly Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala
                85                  90                  95
Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys
            100                 105                 110
Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn
        115                 120                 125
Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser
    130                 135                 140
Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala
145                 150                 155                 160
Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn
                165                 170                 175
Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys
            180                 185                 190
Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Ser Tyr
        195                 200                 205
Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser
    210                 215                 220
Tyr Arg Glu Pro Phe Glu Gln Ser Gly Gly Gly Gly Gly Ala Ala Pro
225                 230                 235                 240
Thr Glu Thr Gln Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn
                245                 250                 255
```

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Leu Cys Thr Val Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser
            260                 265                 270
Asn Cys Ser Leu Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys
        275                 280                 285
Lys Ile Ala Pro Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu
    290                 295                 300
Arg Ile Cys Leu Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu
305                 310                 315                 320
Lys Pro Ser Ile Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp
                325                 330                 335
Pro Glu Ser Ala Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser
            340                 345                 350
Tyr Met Lys Cys Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr
        355                 360                 365
Asn Tyr Thr Leu Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln
    370                 375                 380
Cys Glu Asn Ile Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp
385                 390                 395                 400
Leu Thr Lys Val Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile
                405                 410                 415
Met Val Lys Asp Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val
            420                 425                 430
Pro Leu Thr Ser Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu
        435                 440                 445
Ser Phe His Asn Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn
    450                 455                 460
Phe Ile Ser Arg Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln
465                 470                 475                 480
Thr Glu Thr His Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn
                485                 490                 495
Pro Glu Phe Glu Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro
            500                 505                 510
Gly Val Leu Pro Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr
        515                 520                 525
Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln
    530                 535                 540
Glu Met Ser Ile Gly Lys Lys Arg Asn Ser Thr Thr Gly Asp Lys Thr
545                 550                 555                 560
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
                565                 570                 575
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
            580                 585                 590
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
        595                 600                 605
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
    610                 615                 620
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
625                 630                 635                 640
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
                645                 650                 655
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
            660                 665                 670
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
        675                 680                 685
Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
    690                 695                 700
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
705                 710                 715                 720
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
                725                 730                 735
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
```

```
            740                 745                 750
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
        755                 760                 765
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    770                 775                 780
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<210> 31
<211> 2382
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2379)

<400> 31

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Met Val Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
 1               5                  10                  15

gcc ggc ggc ggg ggc ggg ggc ggg ggc gcc gcg cct acg gaa act cag        96
Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln
            20                  25                  30

cca cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta       144
Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val
        35                  40                  45

ata tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta       192
Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu
    50                  55                  60

tgg tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg       240
Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro
65                  70                  75                  80

gaa act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg       288
Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu
                85                  90                  95

caa gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att       336
Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile
            100                 105                 110

ttg gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct       384
Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala
        115                 120                 125

gtg act gag ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt       432
Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys
    130                 135                 140

tct tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc       480
Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu
145                 150                 155                 160

tac tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc       528
Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile
                165                 170                 175

ttt aga gaa ggc caa tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg       576
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```
Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val
            180                 185                 190

aag gat tcc agt ttt gaa caa cac agt gtc caa ata atg gtc aag gat      624
Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp
        195                 200                 205

aat gca gga aaa att aaa cca tcc ttc aat ata gtg cct tta act tcc      672
Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser
    210                 215                 220

cgt gtg aaa cct gat cct cca cat att aaa aac ctc tcc ttc cac aat      720
Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn
225                 230                 235                 240

gat gac cta tat gtg caa tgg gag aat cca cag aat ttt att agc aga      768
Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg
                245                 250                 255

tgc cta ttt tat gaa gta gaa gtc aat aac agc caa act gag aca cat      816
Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His
            260                 265                 270

aat gtt ttc tac gtc caa gag gct aaa tgt gag aat cca gaa ttt gag      864
Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu
        275                 280                 285

aga aat gtg gag aat aca tct tgt ttc atg gtc cct ggt gtt ctt cct      912
Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro
    290                 295                 300

gat act ttg aac aca gtc aga ata aga gtc aaa aca aat aag tta tgc      960
Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys
305                 310                 315                 320

tat gag gat gac aaa ctc tgg agt aat tgg agc caa gaa atg agt ata     1008
Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile
                325                 330                 335

ggt aag aag cgc aat tcc aca ggc gcg cct agt ggt gga ggt ggc cgg     1056
Gly Lys Lys Arg Asn Ser Thr Gly Ala Pro Ser Gly Gly Gly Gly Arg
            340                 345                 350

ccc gca agc tct ggg aac atg aag gtc ttg cag gag ccc acc tgc gtc     1104
Pro Ala Ser Ser Gly Asn Met Lys Val Leu Gln Glu Pro Thr Cys Val
        355                 360                 365

tcc gac tac atg agc atc tct act tgc gag tgg aag atg aat ggt ccc     1152
Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met Asn Gly Pro
    370                 375                 380

acc aat tgc agc acc gag ctc cgc ctg ttg tac cag ctg gtt ttt ctg     1200
Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu
385                 390                 395                 400

ctc tcc gaa gcc cac acg tgt atc cct gag aac aac gga ggc gcg ggg     1248
Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly
                405                 410                 415

tgc gtg tgc cac ctg ctc atg gat gac gtg gtc agt gcg gat aac tat     1296
Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala Asp Asn Tyr
```

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                420                 425                 430

aca ctg gac ctg tgg gct ggg cag cag ctg ctg tgg aag ggc tcc ttc      1344
Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe
        435                 440                 445

aag ccc agc gag cat gtg aaa ccc agg gcc cca gga aac ctg aca gtt      1392
Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn Leu Thr Val
    450                 455                 460

cac acc aat gtc tcc gac act ctg ctg ctg acc tgg agc aac ccg tat      1440
His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr
465                 470                 475                 480

ccc cct gac aat tac ctg tat aat cat ctc acc tat gca gtc aac att      1488
Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala Val Asn Ile
                485                 490                 495

tgg agt gaa aac gac ccg gca gat ttc aga atc tat aac gtg acc tac      1536
Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr
            500                 505                 510

cta gaa ccc tcc ctc cgc atc gca gcc agc acc ctg aag tct ggg att      1584
Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile
        515                 520                 525

tcc tac agg gca cgg gtg agg gcc tgg gct cag tgc tat aac acc acc      1632
Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr Asn Thr Thr
    530                 535                 540

tgg agt gag tgg agc ccc agc acc aag tgg cac aac tcc tac agg gag      1680
Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser Tyr Arg Glu
545                 550                 555                 560

ccc ttc gag cag tcc gga gac aaa act cac aca tgc cca ccg tgc cca      1728
Pro Phe Glu Gln Ser Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                565                 570                 575

gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa      1776
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            580                 585                 590

ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg      1824
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        595                 600                 605

gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac      1872
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    610                 615                 620

gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag      1920
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
625                 630                 635                 640

cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac      1968
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                645                 650                 655

cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa      2016
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            660                 665                 670
```

```
gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag      2064
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        675                 680                 685

ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg      2112
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
    690                 695                 700

acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc      2160
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
705                 710                 715                 720

agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac      2208
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                725                 730                 735

tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc      2256
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            740                 745                 750

tat agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc      2304
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        755                 760                 765

ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag      2352
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    770                 775                 780

aag agc ctc tcc ctg tct ccg ggt aaa tga                             2382
Lys Ser Leu Ser Leu Ser Pro Gly Lys
785                 790
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<210> 32
<211> 793
<212> PRT
<213> Homo sapiens

<400> 32

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Met Val Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
 1               5                  10                  15
Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln
            20                  25                  30
Pro Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val
        35                  40                  45
Ile Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu
    50                  55                  60
Trp Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro
65                  70                  75                  80
Glu Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu
                85                  90                  95
Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile
            100                 105                 110
Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala
        115                 120                 125
Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys
    130                 135                 140
Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu
145                 150                 155                 160
Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile
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                 165                 170                 175
Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val
            180                 185                 190
Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp
        195                 200                 205
Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser
    210                 215                 220
Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn
225                 230                 235                 240
Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg
                245                 250                 255
Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His
            260                 265                 270
Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu
        275                 280                 285
Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro
    290                 295                 300
Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys
305                 310                 315                 320
Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile
                325                 330                 335
Gly Lys Lys Arg Asn Ser Thr Gly Ala Pro Ser Gly Gly Gly Gly Arg
            340                 345                 350
Pro Ala Ser Ser Gly Asn Met Lys Val Leu Gln Glu Pro Thr Cys Val
        355                 360                 365
Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met Asn Gly Pro
    370                 375                 380
Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu Val Phe Leu
385                 390                 395                 400
Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly Gly Ala Gly
                405                 410                 415
Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala Asp Asn Tyr
            420                 425                 430
Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys Gly Ser Phe
        435                 440                 445
Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn Leu Thr Val
    450                 455                 460
His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser Asn Pro Tyr
465                 470                 475                 480
Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala Val Asn Ile
                485                 490                 495
Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn Val Thr Tyr
            500                 505                 510
Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys Ser Gly Ile
        515                 520                 525
Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr Asn Thr Thr
    530                 535                 540
Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser Tyr Arg Glu
545                 550                 555                 560
Pro Phe Glu Gln Ser Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                565                 570                 575
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            580                 585                 590
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        595                 600                 605
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    610                 615                 620
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
625                 630                 635                 640
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                645                 650                 655
```

```
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                660                 665                 670
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        675                 680                 685
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
    690                 695                 700
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
705                 710                 715                 720
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                725                 730                 735
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                740                 745                 750
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        755                 760                 765
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    770                 775                 780
Lys Ser Leu Ser Leu Ser Pro Gly Lys
785                 790
```